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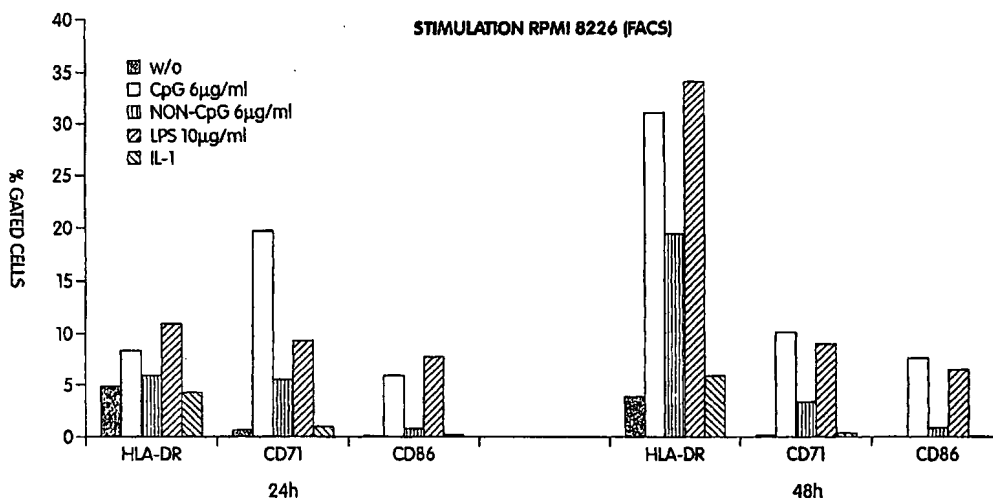
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(54) Title: METHODS AND PRODUCTS FOR IDENTIFICATION AND ASSESSMENT OF TLR LIGANDS



(57) Abstract: The invention provides in part novel screening methods and compositions for identifying and distinguishing between candidate immunomodulatory compounds. The invention further provides methods for assessing biological activity of composition containing a known TLR ligand. These latter methods can be used for quality assessment and selection of various lots of test compositions, including pharmaceutical products for clinical use.



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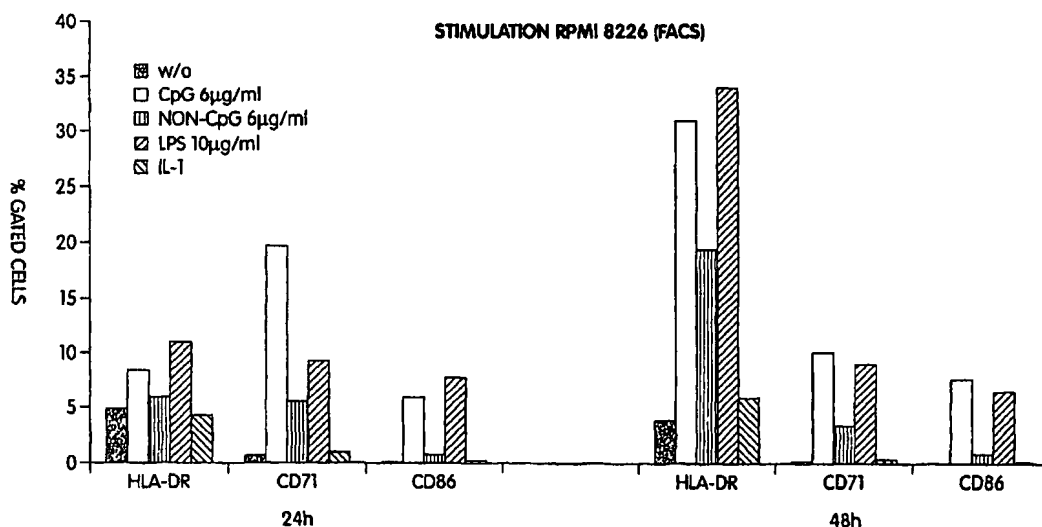
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**METHODS AND PRODUCTS FOR IDENTIFICATION AND ASSESSMENT
OF TLR LIGANDS**

Background of the Invention

5 Nucleic acids with immunostimulatory activity have been identified. The first recognized immunostimulatory motif was the CpG motif in which at least the C of the dinucleotide was unmethylated. It has been postulated that mammalian subjects recognize the unmethylated dinucleotide as being of bacterial origin, and thus mount a heightened immune response following exposure. The ensuing immune response includes both cell mediated and humoral aspects. Since the discovery of the CpG immunostimulatory motif, other immunostimulatory motifs have also been identified including the poly-T and T-rich motifs, the TG motif and the poly-G motif. In some instances, immunostimulation has also been observed in response to exposure to methylated CpG motifs and motif-less nucleic acids having phosphorothioate backbone linkages.

15 The responses induced by immunostimulatory nucleic acids are varied and can include production and secretion of cytokines, chemokines, and other growth factors. The nucleic acids can induce a heightened immune stimulation regardless of whether an antigen is also introduced to the subject. Identification of new motifs as well as of subtle differences between response profiles of different nucleic acids oftentimes can be laborious, and a high throughput system for screening nucleic acids for their ability to be immunostimulatory as well as to determine the profile of responses they induce would be useful.

Summary of the Invention

25 The invention provides in its broadest sense screening methods and tools for identification and discrimination of immunomodulatory molecules and assessment and standardization of samples containing known immunomodulatory molecules. The immunomodulatory molecules can be immunostimulatory or immunoinhibitory, and most preferably are Toll-like receptor (TLR) ligands.

30 In one aspect, the invention provides a screening method for identifying TLR agonists. The method comprises contacting a cell line endogenously expressing at least one TLR with a test compound and measuring a test level of TLR signaling activity, wherein a positive test level is indicative of a TLR agonist (i.e., an immunostimulatory compound). The positive test

level may be apparent without referring to a control. Preferably, however, it is determined relative to a control (i.e., the TLR signaling activity from a reference compound).

In some embodiments, the reference compound is a compound that induces no response (i.e., a zero response) or a minimal response. In this case, a test level that is greater
5 than the reference level is indicative of a compound with TLR signaling activity. More preferably, the reference compound is a compound that induces a positive response (i.e., a non-zero response) and that is immunostimulatory. These reference compounds are referred to herein as negative and positive reference compounds, respectively. If the reference compound is immunostimulatory (i.e., a positive reference compound), a non-zero test level
10 that is lower than the reference level is still indicative of an immunostimulatory test compound. In this latter embodiment, the test compound is less immunostimulatory than the reference compound (for that particular readout), but it is nonetheless immunostimulatory given the non-zero response induced. There may be one or more concurrent or consecutive assays with a negative reference compound, a positive reference compound, or both. The
15 reference may also be a standard curve or data generated previously.

In a related aspect, the screening method involves exposing the same cell to a positive reference compound and a test compound in order to identify a test compound that inhibits the immunostimulatory response of the positive reference compound (i.e., a TLR antagonist or an immunoinhibitory compound).

20 In still a related aspect, the screening method involves exposing the same cells to a positive reference compound and a test compound in order to identify a test compound that enhances the immunostimulatory response of the positive reference compound (i.e., an enhancer).

In both of these latter aspects, the assay requires a co-incubation of the positive
25 reference compound, the test compound and the cells. Separate assays with positive reference compound alone and optionally negative reference compound alone are usually also performed.

The positive reference compound is a known TLR ligand. Non-limiting examples include but are not limited to TLR3 ligands, TLR7 ligands, TLR8 ligands and TLR9 ligands.

30 In some embodiments, the positive reference compound is an immunostimulatory nucleic acid. In some embodiments, the positive reference compound is a CpG nucleic acid, a poly-T nucleic acid, a T-rich nucleic acid or a poly-G nucleic acid. Another example of a positive

reference compound is a nucleic acid comprising a backbone that contains at least one phosphorothioate linkage.

It has been further discovered according to the invention that the RPMI 8226 cell line expresses TLR7 and responds to the imidazoquinoline compound R-848 (Resiquimod) which is known to signal through TLR7 and TLR8. Accordingly, the screening method can be performed using RPMI 8226, Raji or RAMOS cells and an imidazoquinoline compound such as R-848 or R-847 (Imiquimod) as the positive reference compound.

In one embodiment, the test compound is a nucleic acid such as but not limited to a DNA, an RNA and a DNA/RNA hybrid. The test compound may be a nucleic acid that does not comprise motif selected from the group consisting of a CpG motif, a poly-T motif, a T-rich motif and a poly-G motif. The test compound may be a nucleic acid that comprises a phosphorothioate backbone linkage. In another embodiment, the test compound is a non-nucleic acid small molecule. The non-nucleic acid small molecule may be derived from a molecular library. In other embodiments, the test compound comprises amino acids, carbohydrates such as polysaccharides. It may be a hormone or a lipid or contain moieties derived therefrom. In other embodiments, the test compounds are putative ligands for TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, TLR10 or TLR11.

In one embodiment, the cell is a RPMI 8226 cell, a Raji cell, a RAMOS cell, a THP-1 cells, a Nalm cell or a KG-1 cell and the TLR is TLR9. In another embodiment, the cell is a RPMI 8226 cell, a Raji cell or a RAMOS cell and the TLR is TLR7. In yet another embodiment, the cell is a KG-1 cell, a Nalm cell, a Raji cell, a RAMOS cell, a Jurkat cell, a Hela cell, a Hep-2 cell, a Hep-2 cells, a A549 cell, a Bewo cell, an NK-92 cell or an NK-92 MI cell and the TLR is TLR3.

In another embodiment, the cell is an RPMI 8226 cell and the TLR is TLR7 or TLR9. In still another embodiment, the cell is a Raji cell and the TLR is TLR9, TLR7 or TLR3.

Depending upon the embodiment, the TLR signaling activity may be measured or detected in a number of ways. In one embodiment, the TLR signaling activity is measured by cytokine, chemokine, or growth factor secretion. The cytokine secretion may be selected from the group consisting of IL-6 secretion, IL-10 secretion, IL-12 secretion, IFN- α secretion and TNF- α secretion, but is not so limited. The chemokine secretion may be IP-10 secretion or IL-8 secretion, but is not so limited.

In another embodiment, the TLR signaling activity is measured by antibody secretion. The antibody secretion may be IgM secretion, but is not limited to this antibody subtype.

In another embodiment, the TLR signaling activity is measured by phosphorylation. The total level of phosphorylation in the cell or the level of phosphorylation of particular factors in the cell may be measured. These factors are preferably signaling factors and can be selected from the group consisting of IRAK, ERK, MyD88, TRAF6, p38, Jun, c-fos, and subunits of NF- κ B, but are not so limited.

In still a further embodiment, the TLR signaling activity is measured by cell surface marker expression. In one embodiment, the TLR signaling activity is measured by an increase in cell surface marker expression. Examples of cell surface markers to be analyzed include CD71, CD86, HLA-DR, CD80, HLA Class I, CD54 and CD69. In other embodiments, the TLR signaling activity is measured by a decrease in cell surface marker expression. Cell surface marker expression can be determined using flow cytometry. TLR signaling activity can also be measured by protein production (e.g., by Western blot).

In another embodiment, the TLR signaling activity is measured by gene expression. Gene expression profiles may be determined using Northern blot analysis or RT-PCR that uses mRNA or total RNA as a starting material. The gene expression of interest may be that of the chemokines and cytokines and cell surface molecules recited above. Gene expression analysis can be performed using microarray techniques.

In yet another embodiment, the TLR signaling activity is measured by cell proliferation. Cell proliferation assays can be measured in a number of ways including but not limited to ^3H -thymidine incorporation.

In one embodiment, the cell is an RPMI 8226 cell and TLR signaling is indicated by expression of a marker such as CD71, CD86 and/or HLA-DR or by expression, production or secretion of a factor such as IL-8, IL-10, IP-10 and/or TNF- α . Preferably, in this latter embodiment, the RPMI 8226 cell is unmodified. In another embodiment, the cell is a Raji cell and the TLR signaling is indicated by IL-6 or IFN- α 2 expression, production or secretion. In yet another embodiment, the cell is a RAMOS cell and the TLR signaling is indicated by CD80 cell surface expression.

TLR signaling activity can be measured via a native readout or an artificial readout or both. A native readout is one that does not rely on introduction of a reporter construct into the cell of interest.

The cell line may be used in a modified or unmodified form. In one embodiment, the cell line is transfected with a reporter construct. The transfection may be transient or stable. The reporter construct generally comprises a promoter, a coding sequence and a

polyadenylation signal. The coding sequence may comprise a reporter sequence selected from the group consisting of an enzyme (e.g., luciferase, alkaline phosphatase, β -galactosidase, chloramphenicol acetyltransferase (CAT), secreted alkaline phosphatase, etc.), a bioluminescence marker (e.g., green fluorescent protein (GFP, U.S. Patent No. 5,491,084), etc.), a surface-expressed molecule (e.g., CD25), a secreted molecule (e.g., IL-8, IL-12 p40, TNF- α , etc.), and other detectable protein sequences known to those of skill in the art. Preferably, the coding sequence encodes a protein, the level or activity of which can be quantified, with preferably a wide linear range.

In some embodiments, the promoter is a promoter that is responsive to TLR signaling pathways (i.e., a "TLR responsive promoter"). In some embodiments, the promoter contains a binding site for a transcription factor activated upon CpG nucleic acid exposure, such as for example NF- κ B. In other embodiments, the promoter contains a binding site for a transcription factor that is activated by a positive reference compound other than CpG nucleic acids. The transcription factor binding site may be selected from the group consisting of a NF- κ B binding site, an AP-1 binding site, a CRE, a SRE, an ISRE, a GAS, an ATF2 binding site, an IRF3 binding site, an IRF7 binding site, an NFAT binding site, a p53 binding site, an SRF binding site, and a TARE, as well as others known to those of skill in the art.

In another embodiment, the promoter contains a functional promoter element from an IL-1 gene, an IL-6 gene, an IL-8 gene, an IL-10 gene, an IL-12 p40 gene, an IFN- α 1 gene, an IFN- α 4 gene, an IFN- β gene, an IFN- γ gene, a TNF- α gene, a TNF- β gene, an IP-9 gene, an IP-10 gene, a RANTES gene, an ITAC gene, a MCP-1 gene, an IGFBP4 gene, a CD54 gene, a CD69 gene, a CD71 gene, a CD80 gene, a CD86 gene, a HLA-DR gene, and a HLA class I gene.

The TLR responsive promoter may be a TLR1 responsive promoter, a TLR2 responsive promoter, a TLR3 responsive promoter, a TLR4 responsive promoter, a TLR5 responsive promoter, a TLR6 responsive promoter, a TLR7 responsive promoter, a TLR8 responsive promoter, a TLR9 responsive promoter, a TLR10 responsive promoter or a TLR11 responsive promoter.

In these latter embodiments, the cell line may be transfected with a reporter construct having a promoter derived from a particular cytokine, chemokine, or cell surface marker, and a unique reporter coding sequence conjugated thereto. In this way, the readout from a particular reporter construct is a surrogate readout for cytokine, chemokine, or cell surface marker readout. Measuring readout from the reporter coding sequences described herein is in

some instances easier than measuring cytokine or chemokine secretion, or upregulation of a cell surface marker.

In these latter embodiments, the cell line may be transfected with a number of reporter constructs each having a promoter derived from a particular cytokine, chemokine, or cell surface marker, and a unique distinguishable coding sequence conjugated thereto. In these
5 embodiments, multiple readouts are possible from one screen. In other embodiments, multiple native readouts are also possible from one screen.

In a related embodiment, the cell may be further transfected with a nucleic acid that codes for a TLR polypeptide or a fragment thereof. Preferably, the TLR is one that is not
10 endogenously expressed by the cell. As an example, if the cell is an RPMI 8226 cell which has been shown to express TLR7 and TLR9 according to the invention, then it may be modified to express TLRs other than these (e.g., TLR8) in some embodiments. In this aspect, the RPMI 8226 cell is responsive to TLR8 ligands. In preferred embodiments, the TLR is a human TLR (i.e., hTLR).

In another aspect, the invention provides an RPMI 8226 cell transfected with a TLR
15 nucleic acid. In still another embodiment, the TLR nucleic acid is selected from the group consisting of TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR8, TLR10 and TLR11. The encoded TLRs nucleic acids can derive from human or non-human sources. Examples of non-human sources include, but are not limited to, murine, bovine, canine, feline, ovine,
20 porcine, and equine species. Other species include chicken and fish, e.g., aquaculture species. The TLR nucleic acids can also include chimeric sequences consisting of domains originating from different species. In preferred embodiments, the TLR is a human TLR.

In still another aspect, the invention provides kits including the cells lines (e.g., the RPMI 8226 cell line), the reporter constructs and/or expression constructs described above,
25 and instructions for use.

Other aspects of the invention provide methods for analyzing the biological activity of individual lots of material containing previously identified specific TLR ligands (i.e., specific compounds which are ligands for a particular TLR) intended for use as, or for use in the preparation of, pharmaceutical compositions. The methods permit a qualitative and,
30 importantly, a quantitative assessment of biological activity of individual lots of TLR ligands, pre-formulation as well as post-formulation. Such methods are useful in the manufacture and validation of pharmaceutical compositions containing, as an active agent, at least one specific ligand of at least one specific TLR. The specific TLR can be any known TLR, including

without limitation TLR3, TLR7, TLR8 and TLR9. The specific TLR ligand is an isolated TLR ligand, either found in nature or synthetic (not found in nature), including in particular certain nucleic acid molecules and small molecules. Nucleic acid molecules that are specific TLR ligands include synthetic and naturally-occurring oligonucleotides having specific base
5 sequence motifs. Furthermore, specific TLR ligands include both agonists and antagonists of specific TLR.

These methods are to be distinguished from test procedures and acceptance criteria for new drug substances and new drug products which are classified as chemical substances.

Unlike the afore-mentioned test procedures and acceptance criteria, the methods of the instant
10 invention deal specifically with characterizing drug substances and drug products which are classified as oligonucleotides. Oligonucleotides are explicitly excluded in ICH Topic Q6A Specifications: Test Procedures and Acceptance Criteria for New Drug Substances and New Drug Products: Chemical Substances, Step 4 – Consensus Guideline: 6 October 1999, § 1.3.

Further still, the methods of the instant invention are to be distinguished from test
15 procedures and acceptance criteria for biotechnological/biological products. Unlike the afore-mentioned test procedures and acceptance criteria, the methods of the invention deal specifically with characterizing biotechnological/biological products which are classified as DNA products. DNA products are explicitly excluded in ICH Harmonised Tripartite Guideline Specifications: Test Procedures and Acceptance Criteria for
20 Biotechnological/Biological Products, Step 4 – 10 March 1999, § 1.3.

In one aspect, the invention provides a method for quality assessment of a test composition containing a known TLR ligand. The method according to this aspect of the invention involves measuring a reference activity of a reference composition comprising a known TLR ligand, wherein the known TLR ligand is a nucleic acid molecule; measuring a
25 test activity of a test composition comprising the known TLR ligand; and comparing the test activity to the reference activity. In one embodiment the method further involves the step of selecting the test composition if the test activity falls within a predetermined range of variance about the reference activity.

In one embodiment, the reference composition is a first production lot of a
30 pharmaceutical composition comprising the known TLR ligand, and the test composition is a second production lot of a pharmaceutical composition comprising the known TLR ligand. This embodiment is particularly useful as a method for developing and applying acceptance criteria for finished pharmaceutical products containing a known TLR ligand.

In another embodiment, the reference composition is a first in-process lot of a composition comprising the known TLR ligand, and the test composition is a second in-process lot of a composition comprising the known TLR ligand. This embodiment is particularly useful as a method for developing and applying acceptance criteria for raw materials and/or other in-process materials containing a known TLR ligand bound for use in a pharmaceutical product.

In one embodiment according to this aspect of the invention, measuring the reference activity involves contacting the reference composition with an isolated cell expressing a TLR responsive to the known TLR ligand, and measuring the test activity involves contacting the test composition with the isolated cell expressing the TLR responsive to the known TLR ligand. Further, in one embodiment the isolated cell expressing the TLR responsive to the known TLR ligand includes an expression vector for the TLR responsive to the known TLR ligand. Such expression vector, and likewise for any expression vector according to the instant invention, can be introduced into the cell using any suitable method.

In one embodiment, the isolated cell expressing the TLR responsive to the known TLR ligand naturally expresses the TLR responsive to the known TLR ligand. Such a cell can be naturally occurring or it can be a cell line, provided the cell does not include an expression vector introduced into the cell for the purpose of artificially inducing the cell to express or overexpress the TLR.

In one particular embodiment, the isolated cell expressing the TLR responsive to the known TLR ligand is RPMI 8226. In another embodiment, the isolated cell expressing the TLR responsive to the known TLR ligand is Raji, RAMOS, Nalm, THP-1 or KG-1 and the TLR is TLR9. In another embodiment, the isolated cell expressing the TLR responsive to the known TLR ligand is RPMI 8226, Raji or RAMOS and the TLR is TLR7. In yet another embodiment, the isolated cell expressing the TLR responsive to the known TLR ligand is a KG-1 cell, a Nalm cell, a Raji cell, a RAMOS cell, a Jurkat cell, a Hela cell, a Hep-2 cell, a Hep-2 cells, a A549 cell, a Bewo cell, an NK-92 cell or an NK-92 MI cell and the TLR is TLR3.

Further according to this aspect of the invention, in one embodiment measuring the reference activity and measuring the test activity each comprises measuring signaling activity mediated by a TLR responsive to the known TLR ligand. As described in greater detail elsewhere herein, TLR signaling involves a series of intracellular signaling events. These signaling events give rise to various downstream products, including certain transcription

factors (e.g., NF- κ B and AP-1), cytokines, chemokines, etc., which can affect the activity of certain gene promoters. For example, in one embodiment the signaling activity is activity of a reporter gene or reporter construct under the control of a NF- κ B response element.

In other embodiments, the signaling activity is activity of a reporter gene or reporter
5 construct under the control of an interferon-stimulated response element (ISRE); an IFN- α promoter; an IFN- β promoter; an IL-6 promoter; an IL-8 promoter; an IL-12 p40 promoter; a RANTES promoter; an IL-10 promoter or an IP-10 promoter.

In one embodiment, the known TLR ligand is an immunostimulatory nucleic acid. An immunostimulatory nucleic acid can include, without limitation, a CpG nucleic acid. In
10 another embodiment, the known TLR ligand is an immunoinhibitory nucleic acid. When the known TLR ligand is a TLR antagonist (e.g., an immunoinhibitory oligonucleotide), the method according to this aspect of the invention can further involve measuring the reference activity of the reference composition and measuring the test activity of the test composition, each performed in the presence of a known immunostimulatory TLR ligand.

15 In various embodiments, the known TLR ligand is a ligand for a particular TLR. Thus in one embodiment the known TLR ligand is a TLR9 ligand. More specifically, in one embodiment the known TLR ligand is a CpG nucleic acid.

In one embodiment, the known TLR ligand is a TLR3 ligand. Such a ligand can include, for example, a double-stranded RNA or a homolog thereof.

20 In one embodiment, the known TLR ligand is a TLR7 ligand. In one embodiment the known TLR ligand is a TLR8 ligand.

The invention provides in another aspect a method for quality assessment of a test lot of a pharmaceutical product containing a known TLR9 ligand. The method according to this aspect of the invention involves measuring a reference activity of a reference lot of a
25 pharmaceutical product comprising a known TLR9 ligand, wherein the known TLR9 ligand is a nucleic acid molecule; measuring a test activity of a test lot of a pharmaceutical product comprising the known TLR9 ligand; comparing the test activity to the reference activity; and rejecting the test lot if the test activity falls outside of a predetermined range of variance about the reference activity.

30 In one embodiment according to this aspect of the invention, the known TLR9 ligand is an oligonucleotide having a base sequence provided by 5'-TCG TCG TTT TGT CGT TTT GTC GTT-3' (SEQ ID NO:1).

In one embodiment according to this aspect of the invention, the known TLR9 ligand is an oligonucleotide having a base sequence provided by 5'-TCG TCG TTT TGA CGT TTT GTC GTT-3' (SEQ ID NO:139).

5 In one embodiment according to this aspect of the invention, the known TLR9 ligand is an oligonucleotide having a base sequence provided by 5'-TCG TCG TTT TGT CGT TTT TTT CGA-3' (SEQ ID NO:140).

In one embodiment according to this aspect of the invention, the known TLR9 ligand is an oligonucleotide having a base sequence provided by 5'-TCG TCG TTT CGT CGT TTC GTC GTT-3' (SEQ ID NO:141).

10 In one embodiment according to this aspect of the invention, the known TLR9 ligand is an oligonucleotide having a base sequence provided by 5'-TCG TCG TTT CGT CGT TTT GTC GTT-3' (SEQ ID NO:142).

In one embodiment according to this aspect of the invention, the known TLR9 ligand is an oligonucleotide having a base sequence provided by 5'-TCG TCG TTT TTC GGT CGT 15 TTT-3' (SEQ ID NO:143).

In one embodiment according to this aspect of the invention, the known TLR9 ligand is an oligonucleotide having a base sequence provided by 5'-TCG TCG TTT TTC GTG CGT TTT T-3' (SEQ ID NO:144).

20 In one embodiment according to this aspect of the invention, the known TLR9 ligand is an oligonucleotide having a base sequence provided by 5'-TCG TCG TTT TCG GCG GCC GCC G-3' (SEQ ID NO:145).

In one embodiment according to this aspect of the invention, the known TLR9 ligand is an oligonucleotide having a base sequence provided by 5'-TCG TC_G TTT TAC_GGC GCC_GTG CCG-3' (SEQ ID NO:146), wherein every internucleoside linkage is 25 phosphorothioate except for those indicated by “_”, which are phosphodiester.

Each of the limitations of the invention can encompass various embodiments of the invention. It is, therefore, anticipated that each of the limitations of the invention involving any one element or combinations of elements can be included in each aspect of the invention.

Fig. 1 is a bar graph showing cell surface expression of various markers by RPMI 8226 24 hours and 48 hours following stimulation with CpG nucleic acid (SEQ ID NO: 1), non-CpG nucleic acid (SEQ ID NO: 2), LPS and IL-1.

Fig. 2 is a bar graph showing IL-8 production by RPMI 8226 24 hours after exposure to CpG nucleic acid (SEQ ID NO: 1), non-CpG nucleic acid (SEQ ID NO: 2), R-848 and LPS.

Fig. 3 is a bar graph showing IL-6 production by RPMI 8226 24 hours after exposure to CpG nucleic acid (SEQ ID NO: 1), non-CpG nucleic acid (SEQ ID NO: 2), R-848 and LPS.

Fig. 4 is a bar graph showing IP-10 production by RPMI 8226 24 hours after exposure to CpG nucleic acid (SEQ ID NO: 1), non-CpG nucleic acid (SEQ ID NO: 2), R-848 and LPS.

Fig. 5 is a bar graph showing IL-10 production by RPMI 8226 24 hours after exposure to CpG nucleic acid (SEQ ID NO: 1), non-CpG nucleic acid (SEQ ID NO: 2), R-848 and LPS.

Fig. 6 is a dose response curve showing fold induction of IL-8 production 24 hours after exposure to CpG nucleic acid (SEQ ID NO: 1) and non-CpG nucleic acid (SEQ ID NO: 2). The EC₅₀ for CpG nucleic acid is 19 nM and the EC₅₀ for non-CpG nucleic acid is 263 nM.

Fig. 7 is a bar graph showing NF- κ B activation in RPMI 8226 transfected transiently with a NF- κ B-luciferase reporter gene construct as a function of cell density and nucleic acid amount transfected, following exposure to CpG nucleic acid (SEQ ID NO: 1), LPS and TNF- α . NF- κ B activation is measured by luciferase activity.

Fig. 8 is a bar graph showing RT-PCR results from RNA isolated from RPMI 8226 using gene specific primers for TLR7, TLR8 and TLR9 genes.

Fig. 9 is a dose response curve showing IP-10 production induced by SEQ ID NO: 1, and inhibition thereof in the presence of SEQ ID NO: 151, a immunoinhibitory nucleic acid.

Fig. 10 is a bar graph showing the results of a TLR9 RT-PCR analysis of a number of cell lines.

Fig. 11 is a bar graph showing the results of a TLR7 RT-PCR analysis of a number of cell lines.

Fig. 12 is a bar graph showing the results of a TLR3 RT-PCR analysis of a number of cell lines.

Fig. 13 is a bar graph showing the results of a TLR3, TLR7, TLR8 and TLR9 RT-PCR analysis of the Raji cell line.

Fig. 14 is a graph showing IL-6 production by the Raji cell line upon stimulation with various ODN (SEQ ID NO:1; SEQ ID NO:154; SEQ ID NO:158; SEQ ID NO:160; SEQ ID
5 NO:159; SEQ ID NO:161).

Fig. 15 is a bar graph showing IL-6 production of the Raji cell line upon stimulation with poly I:C and R-848.

Fig. 16 is a bar graph showing IFN- α 2 production by the Raji cell line upon stimulation with CpG ODN (SEQ ID NO: 1), R-848 and poly I:C.

Fig. 17 is a bar graph showing CD80 expression (by flow cytometry) by the RAMOS
10 cell line upon stimulation with CpG ODN (SEQ ID NO: 1) and non-CpG ODN (SEQ ID NO: 2).

Fig. 18A is a bar graph showing the induction of NF- κ B by 293 fibroblast cells transfected with human TLR9 in response to exposure to various stimuli, including CpG-
15 ODN, GpC-ODN, LPS, and medium.

Fig. 18B is a bar graph showing the amount of IL-8 produced by 293 fibroblast cells transfected with human TLR9 in response to exposure to various stimuli, including CpG-ODN, GpC-ODN, LPS, and medium.

Fig. 19 is a bar graph showing the induction of NF- κ B-luc produced by stably
20 transfected 293-mTLR9 cells in response to exposure to various stimuli, including CpG-ODN, methylated CpG-ODN (Me-CpG-ODN), GpC-ODN, LPS and medium.

Fig. 20 is a bar graph showing the induction of NF- κ B-luc produced by stably transfected 293-hTLR9 cells in response to exposure to various stimuli, including CpG-ODN, methylated CpG-ODN (Me-CpG-ODN), GpC-ODN, LPS and medium.

Fig. 21 is a series of gel images depicting the results of reverse transcriptase-polymerase chain reaction (RT-PCR) assays for murine TLR9 (mTLR9), human TLR9 (hTLR9), and glyceraldehyde-3-phosphate dehydrogenase (GAPDH) in untransfected control 293 cells, 293 cells transfected with mTLR9 (293-mTLR9), and 293 cells transfected with hTLR9 (293-hTLR9).
30

It is to be understood that the Figures are not required for enablement of the invention.

Brief Description of Sequences

SEQ ID NO:1 is the nucleotide sequence of an immunostimulatory nucleic acid (TLR9 ligand).

SEQ ID NO:2 is the nucleotide sequence of a non-CpG nucleic acid.

SEQ ID NO:3 is the nucleotide sequence of human TLR2 cDNA (U88878).

5 SEQ ID NO:4 is the amino acid sequence of human TLR2 protein (AAC34133).

SEQ ID NO:5 is the nucleotide sequence of murine TLR2 cDNA (AF165189).

SEQ ID NO:6 is the amino acid sequence of murine TLR2 protein (NP_036035).

SEQ ID NO:7 is the nucleotide sequence of human TLR3 cDNA (NM_003265).

SEQ ID NO:8 is the amino acid sequence of human TLR3 protein (NP_003256).

10 SEQ ID NO:9 is the nucleotide sequence of murine TLR3 cDNA (AF355152).

SEQ ID NO:10 is the amino acid sequence of murine TLR3 protein (AAK26117).

SEQ ID NO:11 is the nucleotide sequence of human TLR4 cDNA (U88880).

SEQ ID NO:12 is the nucleotide sequence of human TLR4 cDNA transcript variant 4 (NM_138557).

15 SEQ ID NO:13 is the nucleotide sequence of human TLR4 cDNA transcript variant 2 (NM_138556).

SEQ ID NO:14 is the nucleotide sequence of human TLR4 cDNA transcript variant 1 (NM_138554).

20 SEQ ID NO:15 is the nucleotide sequence of human TLR4 cDNA transcript variant 3 (NM_003266).

SEQ ID NO:16 is the amino acid sequence of human TLR4 protein isoform A (NP_612564).

SEQ ID NO:17 is the amino acid sequence of human TLR4 protein isoform B (NP_612566).

25 SEQ ID NO:18 is the amino acid sequence of human TLR4 protein isoform C (NP_003257).

SEQ ID NO:19 is the amino acid sequence of human TLR4 protein isoform D (NP_612567).

SEQ ID NO:20 is the nucleotide sequence of murine TLR4 cDNA (NM_021297).

30 SEQ ID NO:21 is the nucleotide sequence of murine TLR4 mRNA (AF185285).

SEQ ID NO:22 is the nucleotide sequence of murine TLR4 mRNA (AF110133).

SEQ ID NO:23 is the amino acid sequence of murine TLR4 protein (AAD29272).

SEQ ID NO:24 is the amino acid sequence of murine TLR4 protein (AAF04278).

SEQ ID NO:25 is the nucleotide sequence of human TLR5 cDNA (AB060695).

SEQ ID NO:26 is the amino acid sequence of human TLR5 protein (BAB43558).

SEQ ID NO:27 is the amino acid sequence of human TLR5 protein (O60602).

SEQ ID NO:28 is the amino acid sequence of human TLR5 protein (AAC34136).

5 SEQ ID NO:29 is the nucleotide sequence of murine TLR5 cDNA (AF186107).

SEQ ID NO:30 is the amino acid sequence of murine TLR5 protein (AAF65625).

SEQ ID NO:31 is the nucleotide sequence of human TLR7 cDNA (AF240467).

SEQ ID NO:32 is the nucleotide sequence of human TLR7 cDNA (AF245702).

SEQ ID NO:33 is the nucleotide sequence of human TLR7 cDNA (NM_016562).

10 SEQ ID NO:34 is the amino acid sequence of human TLR7 protein (AAF60188).

SEQ ID NO:35 is the amino acid sequence of human TLR7 protein (AAF78035).

SEQ ID NO:36 is the amino acid sequence of human TLR7 protein (NP_057646).

SEQ ID NO:37 is the amino acid sequence of human TLR7 protein (Q9NYK1).

SEQ ID NO:38 is the nucleotide sequence of murine TLR7 cDNA (AY035889).

15 SEQ ID NO:39 is the nucleotide sequence of murine TLR7 splice variant
(NM_133211).

SEQ ID NO:40 is the nucleotide sequence of murine TLR7 splice variant (AF334942).

SEQ ID NO:41 is the amino acid sequence of murine TLR7 protein (AAK62676).

SEQ ID NO:42 is the amino acid sequence of murine TLR7 protein (AAL73191).

20 SEQ ID NO:43 is the amino acid sequence of murine TLR7 protein (AAL73192).

SEQ ID NO:44 is the amino acid sequence of murine TLR7 protein (NP_573474).

SEQ ID NO:45 is the amino acid sequence of murine TLR7 protein (P58681).

SEQ ID NO:46 is the nucleotide sequence of human TLR8 cDNA (AF245703).

SEQ ID NO:47 is the nucleotide sequence of human TLR8 cDNA (AF246971).

25 SEQ ID NO:48 is the nucleotide sequence of human TLR8 cDNA (NM_138636).

SEQ ID NO:49 is the nucleotide sequence of human TLR8 cDNA (NM_016610).

SEQ ID NO:50 is the amino acid sequence of human TLR8 protein (AAF78036).

SEQ ID NO:51 is the amino acid sequence of human TLR8 protein (AAF64061).

SEQ ID NO:52 is the amino acid sequence of human TLR8 protein (Q9NR97).

30 SEQ ID NO:53 is the amino acid sequence of human TLR8 protein (NP_619542).

SEQ ID NO:54 is the amino acid sequence of human TLR8 protein (NP_057694).

SEQ ID NO:55 is the nucleotide sequence of murine TLR8 cDNA (AY035890).

SEQ ID NO:56 is the nucleotide sequence of murine TLR8 cDNA (NM_133212).

SEQ ID NO:57 is the amino acid sequence of murine TLR8 protein (AAK62677).
SEQ ID NO:58 is the amino acid sequence of murine TLR8 protein (NP_573475).
SEQ ID NO:59 is the amino acid sequence of murine TLR8 protein (P58682).
SEQ ID NO:60 is the nucleotide sequence of human TLR9 cDNA (AF245704).
5 SEQ ID NO:61 is the nucleotide sequence of human TLR9 cDNA (AB045180).
SEQ ID NO:62 is the amino acid sequence of human TLR9 protein (AAF78037).
SEQ ID NO:63 is the amino acid sequence of human TLR9 protein (AAF72189).
SEQ ID NO:64 is the amino acid sequence of human TLR9 protein (AAG01734).
SEQ ID NO:65 is the amino acid sequence of human TLR9 protein (AAG01735).
10 SEQ ID NO:66 is the amino acid sequence of human TLR9 protein (AAG01736).
SEQ ID NO:67 is the amino acid sequence of human TLR9 protein (BAB19259).
SEQ ID NO:68 is the nucleotide sequence of murine TLR9 cDNA (AF348140).
SEQ ID NO:69 is the nucleotide sequence of murine TLR9 cDNA (AB045181).
SEQ ID NO:70 is the nucleotide sequence of murine TLR9 cDNA (AF314224).
15 SEQ ID NO:71 is the nucleotide sequence of murine TLR9 cDNA (NM_031178).
SEQ ID NO:72 is the amino acid sequence of murine TLR9 protein (AAK29625).
SEQ ID NO:73 is the amino acid sequence of murine TLR9 protein (AAK28488).
SEQ ID NO:74 is the amino acid sequence of murine TLR9 protein (BAB19260).
SEQ ID NO:75 is the amino acid sequence of murine TLR9 protein (NP_112455).
20 SEQ ID NO:76 is the nucleotide sequence of human TLR10 cDNA (AF296673).
SEQ ID NO:77 is the amino acid sequence of human TLR10 protein (AAK26744).
SEQ ID NO:78 is the nucleotide sequence of human TLR6 cDNA (AB020807).
SEQ ID NO:79 is the nucleotide sequence of human TLR6 mRNA (NM_006068).
SEQ ID NO:80 is the amino acid sequence of human TLR6 protein (BAA78631).
25 SEQ ID NO:81 is the amino acid sequence of human TLR6 protein (NP_006059).
SEQ ID NO:82 is the amino acid sequence of human TLR6 protein (Q9Y2C9).
SEQ ID NO:83 is the nucleotide sequence of murine TLR6 cDNA (AB020808).
SEQ ID NO:84 is the nucleotide sequence of murine TLR6 cDNA (NM_011604).
SEQ ID NO:85 is the nucleotide sequence of murine TLR6 cDNA (AF314636).
30 SEQ ID NO:86 is the amino acid sequence of murine TLR6 protein (BAA78632).
SEQ ID NO:87 is the amino acid sequence of murine TLR6 protein (AAG38563).
SEQ ID NO:88 is the amino acid sequence of murine TLR6 protein (NP_035734).
SEQ ID NO:89 is the amino acid sequence of murine TLR6 protein (Q9EPW9).

SEQ ID NO:90 is the nucleotide sequence of a consensus sequence for NF- κ B p50 subunit.

SEQ ID NO:91 is the nucleotide sequence of a consensus sequence for NF- κ B p65 subunit.

5 SEQ ID NO:92 is the nucleotide sequence of an example of an NF- κ B p65 subunit binding site.

SEQ ID NO:93 is the nucleotide sequence of an example of a murine CREB binding site.

10 SEQ ID NO:94 is the nucleotide sequence of an example of a murine AP-1 binding site.

SEQ ID NO:95 is the nucleotide sequence of an example of a murine AP-1 binding site.

SEQ ID NO:96 is the nucleotide sequence of an example of an ISRE.

SEQ ID NO:97 is the nucleotide sequence of an example of an ISRE.

15 SEQ ID NO:98 is the nucleotide sequence of an example of an ISRE.

SEQ ID NO:99 is the nucleotide sequence of an example of an ISRE.

SEQ ID NO:100 is the nucleotide sequence of an example of an ISRE.

SEQ ID NO:101 is the nucleotide sequence of an example of an ISRE.

SEQ ID NO:102 is the nucleotide sequence of an example of an ISRE.

20 SEQ ID NO:103 is the nucleotide sequence of an example of an SRE.

SEQ ID NO:104 is the nucleotide sequence of an example of an SRE.

SEQ ID NO:105 is the nucleotide sequence of an example of an SRE.

SEQ ID NO:106 is the nucleotide sequence of an example of an NFAT binding site.

SEQ ID NO:107 is the nucleotide sequence of an example of an NFAT binding site.

25 SEQ ID NO:108 is the nucleotide sequence of an example of an NFAT binding site.

SEQ ID NO:109 is the nucleotide sequence of an example of an NFAT binding site.

SEQ ID NO:110 is the nucleotide sequence of an example of a GAS.

SEQ ID NO:111 is the nucleotide sequence of a p53 binding site consensus sequence.

SEQ ID NO:112 is the nucleotide sequence of an example of a p53 binding site.

30 SEQ ID NO:113 is the nucleotide sequence of an example of a p53 binding site.

SEQ ID NO:114 is the nucleotide sequence of an example of a p53 binding site.

SEQ ID NO:115 is the nucleotide sequence of an example of a p53 binding site.

SEQ ID NO:116 is the nucleotide sequence of an example of a p53 binding site.

SEQ ID NO:117 is the nucleotide sequence of an example of a p53 binding site.

SEQ ID NO:118 is the nucleotide sequence of an example of a TARE (TNF- α response element).

SEQ ID NO:119 is the nucleotide sequence of an example of an SRF binding site.

5 SEQ ID NO:120 is the nucleotide sequence of an example of an SRF binding site.

SEQ ID NO:121 is the nucleotide sequence of the -620 to +50 promoter region of IFN- α 4.

SEQ ID NO:122 is the nucleotide sequence of the -140 to +9 promoter region of IFN- α 1.

10 SEQ ID NO:123 is the nucleotide sequence of the -140 to +9 promoter region of IFN- α 1 (point mutation, AL353732).

SEQ ID NO:124 is the nucleotide sequence of the -280 to +20 promoter region of IFN- β .

15 SEQ ID NO:125 is the nucleotide sequence of the -397 to +5 promoter region of human RANTES (AB023652).

SEQ ID NO:126 is the nucleotide sequence of the -751 to +30 promoter region of human IL-12 p40.

SEQ ID NO:127 is the nucleotide sequence of the -250 to +30 promoter region of human IL-12 p40.

20 SEQ ID NO:128 is the nucleotide sequence of the -288 to +7 promoter region of human IL-6.

SEQ ID NO:129 is the nucleotide sequence of the IL-6 gene promoter from -1174 to +7 (M22111).

25 SEQ ID NO:130 is the nucleotide sequence of the -734 to +44 promoter region derived from human IL-8.

SEQ ID NO:131 is the nucleotide sequence of the -162 to 44 promoter region of human IL-8.

SEQ ID NO:132 is the nucleotide sequence of the -615 to +30 promoter region of human TNF- α .

30 SEQ ID NO:133 is the nucleotide sequence of a promoter region of human TNF- β .

SEQ ID NO:134 is the nucleotide sequence of the -875 to +97 promoter region of human IP-10.

SEQ ID NO:135 is the nucleotide sequence of the -219 to +114 promoter region of human CXCL11 (IP-9).

SEQ ID NO:136 is the nucleotide sequence of the full length promoter region of human CXCL11 (IP-9).

5 SEQ ID NO:137 is the nucleotide sequence of the -289 to +217 promoter region of IGFBP4 (Insulin growth factor binding protein 4).

SEQ ID NO:138 is the nucleotide sequence of the full length promoter region of IGFBP4.

10 SEQ ID NO:139 is the nucleotide sequence of an immunostimulatory nucleic acid.

SEQ ID NO:140 is the nucleotide sequence of an immunostimulatory nucleic acid.

SEQ ID NO:141 is the nucleotide sequence of an immunostimulatory nucleic acid.

SEQ ID NO:142 is the nucleotide sequence of an immunostimulatory nucleic acid.

SEQ ID NO:143 is the nucleotide sequence of an immunostimulatory nucleic acid.

SEQ ID NO:144 is the nucleotide sequence of an immunostimulatory nucleic acid.

15 SEQ ID NO:145 is the nucleotide sequence of an immunostimulatory nucleic acid.

SEQ ID NO:146 is the nucleotide sequence of an immunostimulatory nucleic acid.

SEQ ID NO:147 is the nucleotide sequence of an immunostimulatory methylated CpG nucleic acid.

20 SEQ ID NO:148 is the nucleotide sequence of an immunostimulatory methylated CpG nucleic acid.

SEQ ID NO:149 is the nucleotide sequence of an immunostimulatory methylated CpG nucleic acid.

SEQ ID NO:150 is the nucleotide sequence of an immunostimulatory methylated CpG nucleic acid.

25 SEQ ID NO:151 is the nucleotide sequence of an immunoinhibitory nucleic acid.

SEQ ID NO:152 is the nucleotide sequence of a sense primer for human TLR3.

SEQ ID NO:153 is the nucleotide sequence of an antisense primer for human TLR3.

SEQ ID NO:154 is the nucleotide sequence of a GpC nucleic acid.

SEQ ID NO:155 is the nucleotide sequence of a CpG ODN.

30 SEQ ID NO:156 is the nucleotide sequence of a GpC ODN.

SEQ ID NO:157 is the nucleotide sequence of a Me-CpG ODN.

SEQ ID NO:158 is the nucleotide sequence of a TLR9 ligand.

SEQ ID NO:159 is the nucleotide sequence of a TLR9 ligand.

SEQ ID NO:160 is the nucleotide sequence of a TLR9 ligand.

SEQ ID NO:161 is the nucleotide sequence of a TLR9 ligand.

Detailed Description of the Invention

5 In its broadest sense, the invention relates to screening methods and tools to be used to identify and discriminate between newly discovered immunomodulatory molecules and to compare and standardize compositions of known immunomodulatory molecules. The immunomodulatory molecules are preferably TLR ligands.

Thus, the invention is based in part on the discovery that cell lines expressing
10 endogenous TLR respond to TLR ligands in a manner similar to the response of peripheral blood mononuclear cells (PBMC). PBMC respond to immunomodulatory TLR ligands by modulating one or more parameters including gene expression, cell surface marker expression, cytokine and/or chemokine production and secretion, cell cycle status, phosphorylation status, and the like. TLR ligands can be categorized and distinguished based
15 on the cellular changes they induce (i.e., their induction profiles). The ability of a TLR ligand to provide therapeutic or prophylactic benefit to a subject depends on its induction profile. The ability to screen new TLR ligands for a panel of response indicators or parameters allows for rapid discrimination and categorization of TLR ligands. Moreover, the similarity between the cell line responses and those observed after in vivo administration of the TLR ligand
20 indicates that the cell lines are suitable predictors of in vivo activity. The use of in vitro propagated cell lines additionally overcomes the variability encountered when using freshly isolated PBMC.

The TLR ligands identified according to the invention therefore can be used therapeutically or prophylactically in a more patient- or disorder-specific manner. The
25 invention allows for the tailoring of TLR ligands for particular patients or disorders.

The invention identifies a number of cell lines that can be used to identify TLR ligands based on endogenous TLR expression such as TLR3, TLR7 and TLR9 expression. As an example, the invention is premised in part on the discovery of TLR9 expression in a number of cell lines including RPMI 8226, Raji, RAMOS, THP-1, Nalm-6 and KG-1. Cell lines
30 RPMI 8226, Raji and RAMOS have been determined to express TLR7 according to the invention. Cell lines KG-1 cell, a Nalm cell, a Raji cell, a RAMOS cell, a Jurkat cell, a HeLa cell, a Hep-2 cell, a Hep-2 cells, a A549 cell, a Bewo cell, an NK-92 cell or an NK-92 MI cell have been discovered to express TLR3 according to the invention.

It is further premised in part on the discovery that RPMI 8226 cells respond to the imidazoquinoline compound R-848. Consistent with this latter finding, it was also discovered
5 that RPMI 8226 cells express TLR7.

The invention in other aspects provides for screening methods and tools for verifying and standardizing compositions containing known TLR ligands. These compositions may be for example commercial production lots to be used in a clinical setting. Accordingly, the invention provides methods for standardizing lots of known TLR ligands prior to distribution
10 and use clinically. In this way, production processes can be observed and controlled and substandard production lots can be identified and eliminated prior to shipment.

The methods of the instant invention can be used at any step in the preparation and production of clinical material, i.e., pharmaceutical product. In particular, the methods will find use in characterizing or validating raw materials, in-process materials, finished product
15 materials (e.g., pre-release materials), and post-production materials (e.g., post-release materials). The methods can also be used to validate existing process methods, as well as to validate new or changed process methods used in the production of the pharmaceutical product.

20 Screening Assays Generally

The screening assays provided herein may be used to identify immunomodulatory agents. Immunomodulatory agents are agents that either stimulate or inhibit immune responses in a subject. Accordingly, as used herein, immunomodulation embraces both immunostimulation and immunoinhibition.

25 The screening methods are used to identify TLR agonists and antagonists. The methods can also be used to identify compounds that enhance the immunostimulation induced by a TLR agonist. This latter set of compounds is referred to herein as "enhancers". A TLR agonist is a compound that stimulates TLR signaling activity. A TLR antagonist is a compound that inhibits TLR signaling activity. Agonists are generally referred to herein as
30 immunostimulatory compounds because stimulation of TLR is associated with immune stimulation. Antagonists are generally referred to herein as immunoinhibitory compounds because inhibition of TLR is associated with immune inhibition. TLR antagonists include compounds that reduce (or eliminate completely) the immunostimulation induced by a TLR

agonist. In some embodiments, the agonists, antagonists and enhancers are TLR ligands (i.e., they bind to a TLR). In other embodiments, the test compounds with agonist, antagonist or enhancer activity may act downstream or upstream of the TLR-TLR ligand interaction.

An "immunostimulatory compound" as used herein refers to a natural or synthetic compound that characteristically induces a TLR-mediated response when contacted with a suitable functional TLR polypeptide. In one embodiment the immunostimulatory compound is a natural or synthetic compound that induces a TLR-mediated response when contacted with a cell that naturally or artificially expresses a suitable functional TLR polypeptide. Depending on the aspect of the invention, the cell may be an experimental cell or a primary cell such as a PBMC.

Examples of immunostimulatory compounds include the following immunostimulatory nucleic acids, which are discussed in further detail below:

	5'-TCGTCGTTTTGTCGTTTTGTCGTT-3'	(SEQ ID NO:1)
	5'-TCGTCGTTTTGACGTTTTGTCGTT-3'	(SEQ ID NO:139)
15	5'-TCGTCGTTTTGTCGTTTTTTTCGA-3'	(SEQ ID NO:140)
	5'-TCGTCGTTTCGTCGTTTCGTCGTT-3'	(SEQ ID NO:141)
	5'-TCGTCGTTTCGTCGTTTTGTCGTT-3'	(SEQ ID NO:142)
	5'-TCGTCGTTTTTCGGTCGTTTT-3'	(SEQ ID NO:143)
	5'-TCGTCGTTTTTCGTGCGTTTTT-3'	(SEQ ID NO:144)
20	5'-TCGTCGTTTTCGGCGGCCCGCCG-3'	(SEQ ID NO:145)
	5'-TCGTC_GTTTTAC_GGCGCC_GTGCCG-3'	(SEQ ID NO:146)

Imidazoquinolines are immune response modifiers thought to induce expression of several cytokines including interferons (e.g., IFN- α and IFN- β), TNF- α and some interleukins (e.g., IL-1, IL-6 and IL-12) as well as chemokines (e.g., IP-10 and IL-8). Imidazoquinolines are capable of stimulating a Th1 immune response, as evidenced in part by their ability to induce increases in IgG2a levels. Imidazoquinoline agents reportedly are also capable of inhibiting production of Th2 cytokines such as IL-4, IL-5, and IL-13. Some of the cytokines induced by imidazoquinolines are produced by macrophages and dendritic cells. Some species of imidazoquinolines have been reported to increase NK cell lytic activity and to stimulate B cells proliferation and differentiation, thereby inducing antibody production and secretion. Imidazoquinoline mimics can also be tested using the screening methods.

An "immunoinhibitory compound" as used herein refers to a natural or synthetic compound that characteristically inhibits a TLR-mediated response when contacted with a suitable functional TLR polypeptide. In one embodiment the immunoinhibitory compound is a natural or synthetic compound that inhibits a TLR-mediated response when contacted with a cell that naturally or artificially expresses a suitable functional TLR polypeptide.

In addition to the immunoinhibitory nucleic acids disclosed elsewhere herein, immunoinhibitory compounds and TLR antagonists encompass certain small molecules (chloroquine, quinacrine, 9-aminoacridines and 4-aminoquinolines, and derivatives thereof) described by Macfarlane and colleagues in U.S. Pat. 6,221,882; U.S. Pat. 6,399,630; U.S. Pat. 6,479,504; U.S. Pat. 6,521,637; and published U.S. Pat. application 2002/0151564, the contents of all of which are hereby incorporated by reference in their entirety.

The invention provides in part methods and tools that utilize cell lines, in modified or unmodified form, as surrogates for PBMC. Immunomodulation by TLR ligands can be assessed using one or preferably more parameters including but not limited to cytokine and chemokine secretion, upregulation of cell surface markers, changes in cell proliferation, phosphorylation changes, and the like. These parameters may be native readouts or artificial readouts as described herein.

The cellular response to immunostimulatory nucleic acids by the cell lines described herein (e.g., RPMI 8226, Raji, RAMOS, and the like) so resembles that of PBMC that these cells can be used to identify and differentiate between immunomodulatory compounds based on the extent of the induced response and the particular profile of that response. The invention provides a number of cell lines each with a particular endogenous TLR expression profile, as described herein.

The cell lines can be used to identify immunomodulatory compounds with particular response profiles. As an example, the cell lines can be used to identify molecules that are mimics to known TLR ligands. The cell lines can also be used to identify TLR ligands that trigger some but not necessarily all of the responses induced by known TLR ligands. For example, the cell line can be used to distinguish between compounds based on individual or group cytokine or chemokine secretion, or based on upregulation of one, a subset or all cell surface markers. As an example, in some therapeutic instances, it may be desirable to use a compound that induces the secretion of relatively high levels of chemokine such as IP-10, yet induces only relatively low levels of one or more other factors. The screening methods of the invention allow for the identification of such a compound with this type of induction profile.

It is to be understood that the screening method also can be used to determine effective amounts of known and newly identified immunomodulatory compounds. For example, the EC₅₀ value of a TLR ligand for the production of a particular cytokine or chemokine can be determined, thereby facilitating comparison between different nucleic acids.

5 Generally, these assays require the incubation of cells with a reference compound and a test compound, and an analysis of the readout. Depending on the embodiment, the same cells are exposed to the reference compound and the test compound. An example of this latter embodiment is a screening assay for compounds that enhance the immunostimulatory effects of a TLR agonist. Another example is a screening assay for compounds that inhibit the
10 immunostimulatory effects of a TLR agonist. In both examples, the reference compound is a positive reference compound (i.e., it is itself immunostimulatory).

In other embodiments, particularly those directed at identifying immunostimulatory compounds, separate aliquots from the same cell line (or from the same freshly harvested cell population) are exposed to either the reference compound or the test compound, and the
15 readouts from each are measured and compared to the other. If the reference compound is a negative reference compound (i.e., it is inert and neither immunostimulatory nor immunoinhibitory), then any test level that is greater than the reference level is indicative of a test compound that has at least some immunostimulatory capacity. Generally, the negative reference compound is used to set background levels of immunostimulation or
20 immunoinhibition observed in the absence of the test compound. If the reference compound is a positive reference compound (i.e., it is immunostimulatory), then it is possible to compare and contrast the induction profile of the test compound to that of the reference compound.

In some instances, separate reference assays individually containing a positive and a negative reference compound are performed alongside the test assay. For example, if the test
25 assay is a screen for an immunostimulatory TLR ligand, then reference assays can be a positive reference assay (in which the reference compound is immunostimulatory), a negative reference assay (in which the reference compounds is immunologically inert or neutral), or both. A test compound is defined as immunostimulatory if it induces a response greater than that of the negative reference compound. The level and profile of the immunostimulatory
30 response can be compared to the level and profile induced by the positive reference compound. It is to be understood that a test compound that induces a level of immunostimulation less than that of the positive reference compound may still be considered immunostimulatory according to the invention. Modifications to these screening assays for a

desired readout will be apparent to those of ordinary skill in the art based on the teachings provided herein.

If the test assay is a screen for an immunoinhibitory TLR ligand, then the assay may generally involve co-incubation of the test compound and a positive reference compound.

5 The control assay may include co-incubation of the negative and positive reference compounds. As used herein, co-incubation embraces simultaneous or consecutive addition of the reference and test compounds. The test compound may be added before or after the positive reference compound. An immunoinhibitory test compound may be identified by a diminution of the immunostimulatory response induced by the positive reference compound
10 when in the presence of the test compound. If the level of the response is less in the presence of the test compound, this indicates that the test compound is capable of interfering with the immunostimulatory effects of the positive reference compound. As an example, simultaneous or consecutive addition of a putative immunoinhibitory test compound can reduce the amount of cytokines or chemokines secreted by cells in response to the positive reference compound
15 alone, indicating an inhibition of the immunostimulatory effects of the positive reference compound.

The reference immunoinhibitory compound can be used at one or more concentrations in conjunction with a selected or constant concentration of reference immunostimulatory compound. Under proper conditions, the immunostimulatory effect of the reference
20 immunostimulatory compound will be less in the presence of the immunoinhibitory substance than in the absence of the immunoinhibitory substance. Furthermore, under proper conditions, the immunostimulatory effect of the reference immunostimulatory compound will decrease with increasing concentration of the immunoinhibitory substance.

The breadth of response by the cell line to immunomodulatory compounds, and its
25 facile manipulation, allows for the identification of novel compounds. The cell line allows the rapid discovery of such compounds given that it lends itself to high throughput screening methods such as those provided herein. These methods and compositions are described in greater detail below. The invention therefore provides screening methods that utilize cell lines that either endogenous express TLRs such as the RPMI 8226 cell line as well as cell
30 lines that have been modified to express TLRs. The invention further provides compositions that comprise such cell lines.

The verification and standardization methods of the invention generally involve assays in which an isolated cell expressing a functional TLR is contacted with each of two

compositions, each composition containing a known ligand for the TLR. One composition is a reference composition, and the assay using the reference composition yields a reference activity. The second composition is a test composition, and the assay using the test composition yields a test activity. The two contacting steps can be performed on separate
5 cells that are alike, and typically will be performed on separate populations of cells that are alike. For example, the separate cells or the separate populations of cells can be drawn from a single population of cells. In typical usage according to this embodiment, the reference and test activities are measured essentially concurrently, although the use of historical reference activity is also contemplated by the methods of the invention. As an alternative, the two
10 contacting steps can be performed on a single cell or on a single population of cells, usually in an essentially concurrent manner when it is desirable to have competition between reference and test compositions. In one embodiment the known TLR ligand is a nucleic acid molecule.

The assays of the invention are performed under specific conditions so that comparison can be made between reference and test activities or levels. The results of the
15 comparison can be used as a basis upon which to accept or reject the test material as suitable for its intended use.

The biological characterization of the reference composition will generally entail a series of biological activity measurements of the reference composition using a single assay under defined conditions in order to define a range of inter-test variance. The range of inter-
20 test variance so obtained using reference composition can be used to define an acceptable range of variance within which a subsequent test measurement must fall in order to satisfy quality standards. Such a range of acceptable variance can serve as a basis for developing predetermined range of variance about the reference activity, i.e., acceptance criteria for a particular test composition or test lot. For example, a particular reference composition can be
25 assayed under defined conditions in a number of independent measurements and found to yield a result expressed as 100 ± 5 units of activity. Under this same example, a subsequent test measurement of a test composition performed using the same assay and defined conditions is found to yield 97 units of activity. The activity of the test composition under this example thus yielded a result that falls within the normal range of inter-test variance
30 observed for the reference composition. Accordingly, the test material under this example could be selected on the basis of the test activity falling within a predetermined range of variance about the reference activity. In short, the test material can be deemed acceptable

provided the test activity falls within a predetermined range of activity that is related to the activity of the reference material.

In one embodiment, the methods of the invention provide for comparison between a reference lot of a particular TLR ligand and a test lot of the same particular TLR ligand. Such comparison is useful for quality control assessment of the test lot of material, also referred to herein as validation, e.g., product validation. Such comparison is also useful for process validation.

In another embodiment, the methods of the invention provide for comparison between a reference lot of a particular TLR ligand and a test lot of a different TLR ligand. In a simple example, where a test TLR ligand (T) is expected to have little or no activity characteristic of reference TLR ligand (R), comparison can be made between T and R to confirm the lack of R-like activity possessed by T. In a more complex example, where a test TLR ligand (C) is capable of exerting two different effects, wherein each effect is characteristic of one of two different classes of TLR ligand and is best characterized by one of two different reference TLR ligands (A and B), the test TLR ligand (C) can be compared with either of the two reference TLR ligands (A or B). In this second example, test composition C could be found, for example, to possess 50 percent A-like activity compared with reference A and 70 percent B-like activity compared with reference B. Test composition C could thus independently meet or fail to meet predetermined standards for each of A-like activity and B-like activity. Such comparison is also useful for quality control assessment of the test lot of material, e.g., product validation. Of course test TLR ligand C can alternatively or additionally be compared against reference TLR ligand C, as described in the preceding paragraph.

To facilitate the methods of the invention, certain conditions for carrying out the assays are standardized and used for measurements of both reference activity and test activity. In this way direct comparison between reference activity and test activity can be made readily. Conditions that can be standardized and used in this manner can include, without limitation, readout, temperature, media characteristics, duration (time between introduction of reference composition or test composition and activity measurement), methods of sampling, etc. In some embodiments the methods of the invention can be at least partially automated in order to increase throughput and/or to reduce inter-test variability. For example, robotic devices and workstations with the capacity to dispense and/or sample fluids in a set or programmable fashion are now well known in the art and can be used in performing the methods of the instant invention.

In one embodiment a standard curve of reference composition activity is employed. Typically the standard curve is generated by selecting conditions including concentration of the reference composition such that the dose-response curve is essentially linear (and the slope is non-zero) over a range of concentrations that includes the effective concentration at which activity is 50 percent of maximum (EC50). In one embodiment the standard curve spans a range of concentrations defined by $EC50 \pm 1 \log$ concentration, e.g., $1 \times 10^{-7} \text{ M} - 1 \times 10^{-5} \text{ M}$, where EC50 is $1 \times 10^{-6} \text{ M}$. In another embodiment the standard curve spans a broader range of concentrations defined by $EC50 \pm 2 \log$ concentration, e.g., $1 \times 10^{-8} \text{ M} - 1 \times 10^{-4} \text{ M}$, where EC50 is $1 \times 10^{-6} \text{ M}$. In yet another embodiment the standard curve spans a narrower range of concentrations defined by $EC50 \pm 0.5 \log$ concentration, e.g., $3.16 \times 10^{-7} \text{ M} - 3.16 \times 10^{-6} \text{ M}$, where EC50 is $1 \times 10^{-6} \text{ M}$. The foregoing embodiments are intended to be exemplary and not limiting in any way. One of skill in the art will be able to select, for a given reference composition and without undue experimentation, an appropriate range of concentrations about some middle value in order to generate an essentially linear standard curve with a non-zero slope.

In one embodiment a non-linear standard curve of reference and test composition activity is employed. The standard curve can be generated by selecting conditions including concentrations of the reference composition such that the dose-response curve is sigmoidal and the EC50 value can be determined. Comparison of reference and test activity can be done by comparing, e.g., the EC50 values of both curves. Concentration range is chosen to yield a complete sigmoidal response, e.g., concentration should include $EC50 \pm 3 \log$ concentration or $EC50 \pm 4 \log$ concentration. In the case of testing an inhibitory compound the value determined would be the IC50, i.e., concentration where inhibition of the stimulatory signal is half-maximal.

The methods of the invention can be adapted to be automated or at least partially automated methods, as well as to parallel array or high throughput format methods. For example, the assays can be set up using multiwell plates in which cells are dispensed in individual wells and reagents are added in a systematic manner using a multiwell delivery device suited to the geometry of the multiwell plate. Manual and robotic multiwell delivery devices suitable for use in a high throughput screening assay are known by those skilled in the art. Each well or array element can be mapped in a one-to-one manner to a particular test condition, such as the test compound. Readouts can also be performed in this multiwell array, preferably using a multiwell plate reader device or the like. Examples of such devices are

known in the art and are available through commercial sources. Sample and reagent handling can be automated to further enhance the throughput capacity of the screening assay, such that dozens, hundreds, thousands, or even millions of parallel assays can be performed in a day or in a week. Fully robotic systems are known in the art for applications such as generation and analysis of combinatorial libraries of synthetic compounds. See, for example, U.S. Pat. Nos. 5,443,791 and 5,708,158.

Cell lines

The screening methods may use experimental cells. As used herein, an experimental cell is a non-primary cell (i.e., it is not a cell that has been recently harvested from a subject). It excludes, for example, freshly harvested PBMCs. An experimental cell includes a cell from a cell line such as the RPMI 8226 cell line.

In certain embodiments, the cell naturally expresses a functional TLR. In one embodiment relating to the verification and standardization aspects of the invention, the cell may be a PBMC, preferably a PBMC freshly harvested from a subject.

Cells that would be suitable for identification of TLR agonists, antagonists or enhancers according to the invention may possess one or more particular attributes. These attributes include but are not limited to being of human origin, being an immortalized stable cell line, endogenously expressing at least one functional TLR or a combination of functional TLRs, having intact signaling mechanisms, having intact uptake mechanisms, being able to upregulate cytokines, chemokines or cell surface markers, deriving from normal human B cells or from myeloma or B cell leukemia, deriving from human plasmacytoid and myeloid dendritic cells, and readily activatable by TLR ligands such as TLR7 ligands, TLR8 ligands or TLR9 ligands such as CpG nucleic acids or nucleic acids having other immunostimulatory sequence motifs or small molecules such as imidazoquinoline compounds.

In some embodiments, the cell line is the Raji cell line which expresses TLR3, TLR7 and TLR9. This latter cell line secretes, for example, IL-6 and IFN- α 2 upon CpG nucleic acid exposure. In other embodiments, the cell line is RPMI 8226 which expresses TLR7 and TLR9. Upon CpG nucleic acid exposure, this cell line expresses, produces and/or secretes IL-8, IL-10, IP-10 and TNF- α . It also expresses at its cell surface CD86, HLA-DR and CD71. In yet other embodiments, the cell line is the RAMOS cell line which expresses TLR3, TLR7 and TLR9. This cell line at least induces CD80 cell surface expression in response to CpG nucleic acid exposure.

The cell lines have been observed to respond in a concentration dependent manner to TLR ligands such as but not limited to CpG nucleic acids and some non-CpG nucleic acids including T-rich nucleic acids, poly-T nucleic acids and poly-G nucleic acids. The highest responses have been observed using CpG nucleic acids.

5 The screening methods employ a variety of cell lines as shown in the Examples. These include A549 (human lung carcinoma, ATCC CCL-185), BeWo (human choriocarcinoma, ATCC CCL-98), HeLa (human cervix carcinoma, ATCC CCL-2), Hep-2 (human cervix carcinoma, ATCC CCL-23), KG-1 (human acute myeloid leukemia, ATCC CCL-246), MUTZ-3 (human acute myelomonocytic leukemia, German Collection of Cell
10 lines and Microorganisms (DSZM) ACC-295), Nalm-6 (human B cell precursor leukemia, DSZM ACC-128), NK-92 (human Natural killer cell line, ATCC CRL-2407), NK-92 MI (IL-2 independent human Natural killer cell line, ATCC CRL-2408), Raji (human B lymphocyte Burkitt's lymphoma, ATCC CCL-86), RAMOS (B lymphocyte Burkitt's lymphoma, ATCC CRL-1596), RPMI 8226 (human B lymphocyte multiple myeloma, ATCC CCL-155), THP-1
15 (human acute monocytic leukemia, ATCC TIB 202), U937 (human lymphoma, ATCC CRL-1593.2) and Jurkat (human T cell leukemia, ATCC TIB 152).

As shown in the Examples, each of the afore-mentioned cell lines has a particular endogenous TLR expression profile which dictates its suitability in a particular screening assay.

20 A cell that artificially expresses a functional TLR can be a cell that does not express the functional TLR but for a transfected TLR expression vector. For example, human 293 fibroblasts (ATCC CRL-1573) do not express TLR7, TLR8 or TLR9, and they express very little TLR3. As described in the examples below, such cells can be transiently or stably transfected with suitable expression vector (or vectors) so as to yield cells that do express
25 TLR3, TLR7, TLR8, TLR9, or any combination thereof. Alternatively, a cell that artificially expresses a functional TLR can be a cell that expresses the functional TLR at a significantly higher level with the TLR expression vector than it does without the TLR expression vector. Transfected cells are considered modified cells, as used herein.

30 A cell that artificially expresses an expression or reporter construct is preferably stably transfected.

RPMI

The RPMI 8226 cell line is a human multiple myeloma cell line. The cell line was established from the peripheral blood of a 61 year old man at the time of diagnosis for multiple myeloma (IgG lambda type). RPMI 8226 was previously reported as responsive to CpG nucleic acids as evidenced by the production and secretion of IL-6 protein and production of IL-12p40 mRNA. (Takeshita et al. (2000), *Eur. J. Immunol.* 30, 108-116, and Takeshita et al. (2000) *Ibid.* 30, 1967-1976) Takeshita et al. however used the cell line solely to study promoter constructs in order to identify transcription factor binding sites important for CpG nucleic acid signaling. It is now known according to the invention that the cell line produces a number of other chemokines and cytokines including IL-8, IL-10 and IP-10. It has also been discovered according to the invention that the cell line responds to immunostimulatory nucleic acids by upregulating cell surface expression of particular markers. Many of these markers, including CD71, CD86 and HLA-DR, are similarly upregulated in PBMCs exposed to immunostimulatory nucleic acids. This has been observed using flow cytometric analysis of the cell line following CpG nucleic acid exposure. In other aspects of the invention, the cell line can be used in similar screening assays that involve secretion of IL-6, IL-12 and/or TNF- α .

It has recently been discovered that R-848 mediates its immunostimulatory effects via other TLR family members, namely TLR7 and TLR8. TLR7 has previously been found expressed on human B cells. It has now also been discovered according to the invention that RPMI 8226 expresses TLR9 as well as TLR7, thus making it a suitable cell line for identifying immunostimulatory nucleic acid and/or imidazoquinoline (e.g., R-848) mimics or other small molecules that also signal through TLR7 and/or TLR9. Incubation of RPMI 8226 cells with the imidazoquinoline R-848 (Resiquimod) induces for example IL-8, IL-10 and IP-10 production.

Known TLR Ligands

Ligands for many but not all of the TLRs have been described. For instance, it has been reported that TLR1 and TLR2 signals in response to peptidoglycan and lipopeptides. Yoshimura A et al. (1999) *J Immunol* 163:1-5; Brightbill HD et al. (1999) *Science* 285:732-6; Aliprantis AO et al. (1999) *Science* 285:736-9; Takeuchi O et al. (1999) *Immunity* 11:443-51; Underhill DM et al. (1999) *Nature* 401:811-5. TLR4 has been reported to signal in response to lipopolysaccharide (LPS). Hoshino K et al. (1999) *J Immunol* 162:3749-52; Poltorak A et al. (1998) *Science* 282:2085-8; Medzhitov R et al. (1997) *Nature* 388:394-7. Bacterial

flagellin has been reported to be a natural ligand for TLR5. Hayashi F et al. (2001) *Nature* 410:1099-1103. TLR6, in conjunction with TLR2, has been reported to signal in response to proteoglycan. Ozinsky A et al. (2000) *Proc Natl Acad Sci USA* 97:13766-71; Takeuchi O et al. (2001) *Int Immunol* 13:933-40.

5 TLR9 is a receptor for CpG DNA. Hemmi H et al. (2000) *Nature* 408:740-5. Other TLR9 ligands are described herein under "Immunostimulatory Nucleic Acids". Certain imidazoquinoline compounds having antiviral activity are ligands of TLR7 and TLR8. Imidazoquinolines are potent synthetic activators of immune cells with antiviral and antitumor properties. R-848 is a ligand for human TLR7 and TLR8. Jurk M et al. (2002) *Nat Immunol*
10 3:499. Ligands of TLR3 include poly(I:C) and double-stranded RNA (dsRNA). Alexopoulou et al. (2001) *Nature* 413:732-738. For purposes of this invention, poly(I:C) and double-stranded RNA (dsRNA) are classified as oligonucleotide molecules. TLR3 may have a role in host defense against viruses.

15 Reference and Test Compounds

A test and/or reference compound can be a nucleic acid such as an oligonucleotide or a polynucleotide, an oligopeptide, a polypeptide, a lipid such as a lipopolysaccharide, a carbohydrate such as an oligosaccharide or a polysaccharide, or a small molecule.

Alternatively, these compounds may also comprise or be synthesized from elements such as
20 amino acids, carbohydrates, hormones, lipids, organic molecules, and the like.

Small molecules in general include naturally occurring, synthetic, and semisynthetic organic and organometallic compounds with molecular weight less than about 2.5 kDa. Examples of small molecules include most drugs, subunits of polymeric materials, and analogs and derivatives thereof.

25 Some specific examples of small molecules include the imidazoquinolines. As used herein, an imidazoquinoline includes imidazoquinoline amines (imidazoquinolinamines), imidazopyridine amines, 6,7-fused cycloalkylimidazopyridine amines, and 1,2 bridged imidazoquinoline amines. These compounds have been described in U.S. Pat. Nos. 4,689,338; 4,929,624; 5,238,944; 5,266,575; 5,268,376; 5,346,905; 5,352,784; 5,389,640;
30 5,395,937; 5,482,936; 5,494,916; 5,525,612; 6,039,969 and 6,110,929. Particular species of imidazoquinoline agents include resiquimod (R-848; S-28463; 4-amino-2-ethoxymethyl- α,α -dimethyl-1*H*-imidazo[4,5-*c*]quinoline-1-ethanol); and imiquimod (R-837; S-26308; 1-(2-methylpropyl)-1*H*-imidazo[4,5-*c*]quinoline-4-amine). Further examples of specific small

molecules include 4-aminoquinoline and derivatives thereof, 9-aminoacridine and derivatives thereof, and additional compounds disclosed in U.S. Pat. Nos. 6,221,882; 6,399,630; 6,479,504; and 6,521,637; and published U.S. Pat. Application No. 2002/0151564 A1, the entire contents of which are hereby incorporated by reference.

5 The test and reference compounds may be formulated for pharmaceutical use or not. For example, a test compound not formulated for pharmaceutical use can be a compound (e.g., a lot or batch of the compound) under evaluation for possible use in preparing a pharmaceutical formulation of the compound.

10 A reference compound, as used herein, is a compound having a known activity in the presence of a TLR. The reference compound may stimulate TLR signaling (and is therefore regarded as a positive reference compound), or it may be inert in the presence of a TLR (and is therefore regarded as a negative reference compound). If it is a positive reference compound, it need not be the best known stimulator of TLR signaling (i.e., it is possible that other reference compounds and even test compounds will stimulate TLR signaling to a greater
15 extent). The readout of the screening assay may simply be stated relative to the level of signaling that occurs in the presence of the reference compound. Preferably, the reference compound is analyzed prior to the screening assay in order to determine its level of activity on a TLR. In some aspects of the invention, the reference compound and the test compound will be assayed separately (i.e., in separate wells); in other aspects, the reference compound and
20 the test compound will be assayed together (i.e., in the same well). These latter aspects are designed to measure the ability of a test compound to modulate the activity of the reference compound. The activity of the test compound and the reference compound combined (i.e., when assayed together in the same well) may be the same as that of the positive reference compound alone, indicating at a minimum that the test compound is not inhibitory; or it may
25 be less than that of the positive reference compound, indicating at a minimum that it is inhibitory to the effect of the reference compound; or it may be additive or synergistic possibly indicating that the test compound is an enhancer. The effect of an enhance may be due to its ability to stimulate TLR signaling independently of the positive reference compound.

30 A "reference composition" as used herein refers to a composition that includes a reference compound and optionally another agent, e.g., a pharmaceutically acceptable carrier and/or another biologically active agent. A reference compound may be an immunostimulatory compound or it may be an immunoinhibitory compound.

As discussed further below, in some aspects of the invention the reference compositions include both finished products, e.g., finished pharmaceutical products, as well as raw materials and other in-process materials used for the preparation of such finished products, all of which contain a known TLR ligand. As used herein, a "production lot" shall refer to a batch or lot of a completed product prepared for release as clinical material, e.g., a pharmaceutical product. As used herein, an "in-process lot" shall refer to a batch or lot of unfinished product that is prepared in the course of making a production lot; an "in-process lot" shall also refer to a batch or lot of raw material provided for use in the production of a production lot.

In some aspects of the invention, the reference compositions of the invention are highly characterized in terms of their chemical, physical, and biological properties. A reference composition will be a specific composition previously determined to have a specific activity, or range of specific activity, of the particular known TLR ligand present in the composition. As used herein, "specific activity" refers to an amount of activity per unit mass or per unit volume of the reference composition as a whole, as determined using a defined assay under defined conditions. In one embodiment the reference composition is a representative sample of a particular lot or batch of a specific TLR ligand. In one embodiment the reference composition is a representative sample of a particular lot or batch of a specific TLR ligand formulated for pharmaceutical use, e.g., a sterile solution of the TLR ligand at a determined concentration or activity.

At least the following parameters are typically very well defined for a given reference composition: chemical formula of the active ingredient TLR ligand (e.g., nucleobase sequence and type of backbone of a nucleic acid; structural formula of a small molecule); concentration; diluent composition; and purity. Such parameters as purity and concentration can be determined using any appropriate physicochemical method, e.g., optical spectroscopy including absorbance at one or more specified wavelengths; nuclear magnetic resonance (NMR) spectroscopy; mass spectrometry (MS), including matrix-assisted laser desorption/ionization mass spectrometry (MALDI-MS); melting point; specific gravity; chromatography including as appropriate high pressure liquid chromatography (HPLC), one- and two-dimensional polyacrylamide gel electrophoresis (PAGE), capillary electrophoresis, and the like; as well as other methods known to those of skill in the art.

Reference compositions can also be very well characterized in terms of their biological activity, independent of the methods of the invention, although the methods of the

invention generally include such characterization, at least in part. A reference composition can be very well characterized in terms of its biological activity by characterizing, both qualitatively and quantitatively, the response by sensitive cells to the reference composition under defined conditions. For example, a reference composition can be a specific CpG oligonucleotide such as SEQ ID NO:1 which in a specific assay and under specific conditions of temperature, concentration, duration of contact between the CpG oligonucleotide and a population of TLR9-expressing cells, and particular readout, reliably yields a specific result or range of results. Results can be expressed in any suitable manner, but can include results expressed on a per-cell basis, e.g., picograms of particular cytokine per cell per hour of contact with the reference composition. Reference compositions can be very well characterized in terms of their biological activity according to one or more parameters, for example, according to their capacity to induce each of a plurality of cytokines.

The methods of the invention also involve measurement of a test activity of a test composition containing a known TLR ligand. A "test composition" as used herein refers to a composition that includes a test compound and optionally another agent, e.g., a pharmaceutically acceptable carrier and/or another biologically active agent. A test compound can be an immunostimulatory compound or it can be an immunoinhibitory compound. In some aspects of the invention, the test compound is a known TLR ligand. Test compositions of the invention may comprise known TLR agonist or TLR antagonist compounds, generally but not necessarily nominally the same as the reference compositions against which comparison is to be made according to some aspects of the invention. Thus test compositions may encompass immunostimulatory compounds, immunoinhibitory compounds, known TLR ligands, finished pharmaceutical products, and raw materials and other in-process materials used for the preparation of such finished products.

Unlike a reference composition, a test composition is not characterized at all, or is only partially characterized, or is not as well characterized as the reference composition, in terms of its chemical, physical, or (most particularly) biological properties. The methods of the invention permit further characterization of the test composition by comparison with a reference composition. In some aspects, a test composition will be a specific composition previously determined to be a ligand of a specific TLR. In one embodiment the test composition is a representative sample of a particular lot or batch of a specific TLR ligand. In one embodiment the test composition is a representative sample of a particular lot or batch of

a specific TLR ligand formulated for pharmaceutical use, e.g., a sterile solution of the TLR ligand at a determined concentration or activity.

Immunostimulatory and Immunoinhibitory Nucleic Acids

5 Nucleic acids useful as reference compounds and as test compounds in the methods of the invention include single- and double-stranded natural and synthetic nucleic acids, including those with phosphodiester, stabilized, and chimeric backbones. Also encompassed are at least the following classes of nucleic acids, which are described in detail below: immunostimulatory CpG nucleic acids (CpG nucleic acids), including but not limited to types
10 A, B, and C; immunostimulatory non-CpG nucleic acids, including without limitation methylated CpG nucleic acids, T-rich nucleic acids, TG-motif nucleic acids, CpI motif nucleic acids, and poly-G nucleic acids; and immunoinhibitory nucleic acids. Nucleic acids useful as reference compounds and as test compounds in the methods of the invention also include nucleic acids with modified backbones, including "soft" and "semi-soft" oligonucleotides as
15 described herein. As will be appreciated from the descriptions below, certain of these various classes of nucleic acids can coexist in a given nucleic acid molecule.

A "nucleic acid" as used herein with respect to test compounds and reference compounds used in the methods of the invention, shall refer to any polymer of two or more individual nucleoside or nucleotide units. Typically individual nucleoside or nucleotide units
20 will include any one or combination of deoxyribonucleosides, ribonucleosides, deoxyribonucleotides, and ribonucleotides. The individual nucleotide or nucleoside units of the nucleic acid can be naturally occurring or not naturally occurring. For example, the individual nucleotide units can include deoxyadenosine, deoxycytidine, deoxyguanosine, thymidine, and uracil. In addition to naturally occurring 2'-deoxy and 2'-hydroxyl forms,
25 individual nucleosides also include synthetic nucleosides having modified base moieties and/or modified sugar moieties, e.g., as described in Uhlmann E et al. (1990) *Chem Rev* 90:543-84. The linkages between individual nucleotide or nucleoside units can be naturally occurring or not naturally occurring. For example, the linkages can be phosphodiester, phosphorothioate, phosphorodithioate, phosphoramidate, as well as peptide linkages and other
30 covalent linkages, known in the art, suitable for joining adjacent nucleoside or nucleotide units. The linkages can also be mixed in a single polymer (e.g., a semi-soft backbone). The nucleic acid test compounds and nucleic acid reference compounds typically range in size from 3-4 units to a few tens of units, e.g., 18-40 units.

In some embodiments the nucleic acids are oligonucleotides made up of 2 to about 100 nucleotides, and more typically 4 to about 40 nucleotides. Oligonucleotides composed exclusively of deoxynucleotides are termed oligodeoxyribonucleotides or, equivalently, oligodeoxynucleotides (ODN).

5 A CpG nucleic acid is an immunostimulatory nucleic acid which contains a cytosine-guanine (CG) dinucleotide, the C residue of which is unmethylated. The effects of CpG nucleic acids on immune modulation have been described extensively in U.S. Pat. Nos. 6,194,388; 6,207,646; 6,214,806; 6,218,371; 6,239,116; and 6,339,068; and published patent applications, such as PCT/US95/01570 (WO 96/02555); PCT/US98/04703 (WO 98/40100);
10 and PCT/US99/09863 (WO 99/56755). The entire contents of each of these patents and published patent applications is hereby incorporated by reference. The entire immunostimulatory nucleic acid can be unmethylated or portions can be unmethylated, but at least the C of the 5'-CG-3' must be unmethylated. The CpG nucleic acid sequences of the invention include, without limitation, those broadly described above as well as those disclosed
15 in U.S. Pat. Nos. 6,207,646 and 6,239,116.

In one embodiment the CpG nucleic acid has a base sequence provided by 5'-TCGTCGTTTTGTCGTTTTGTCGTT-3' (SEQ ID NO:1).

In one embodiment the CpG nucleic acid has a base sequence provided by 5'-TCGTCGTTTTGACGTTTTGTCGTT-3' (SEQ ID NO:139).

20 In one embodiment the CpG nucleic acid has a base sequence provided by 5'-TCGTCGTTTTGTCGTTTTTTTCGA-3' (SEQ ID NO:140).

In one embodiment the CpG nucleic acid has a base sequence provided by 5'-TCGTCGTTTCGTCGTTTCGTCGTT-3' (SEQ ID NO:141).

25 In one embodiment the CpG nucleic acid has a base sequence provided by 5'-TCGTCGTTTCGTCGTTTTGTCGTT-3' (SEQ ID NO:142).

In one embodiment the CpG nucleic acid has a base sequence provided by 5'-TCGTCGTTTTTCGGTCGTTTT-3' (SEQ ID NO:143).

In one embodiment the CpG nucleic acid has a base sequence provided by 5'-TCGTCGTTTTTCGTGCGTTTTT-3' (SEQ ID NO:144).

30 In one embodiment the CpG nucleic acid has a base sequence provided by 5'-TCGTCGTTTTTCGGCGGCCCGCCG-3' (SEQ ID NO:145).

In one embodiment the CpG nucleic acid has a base sequence provided by 5'-TCGTC_GTTTTAC_GGCGCC_GTGCCG-3' (SEQ ID NO:146).

The oligonucleotides described by SEQ ID NOs: 1, 139-145 are fully stabilized phosphorothioate backbone ODN. The oligonucleotide of SEQ ID NO:146 has a chimeric backbone in which all internucleoside linkages are phosphorothioate except for those indicated by “_”, which are phosphodiester.

5 CpG nucleic acids have been further classified by structure and function into at least the following three types, all of which are intended to be encompassed within the methods of the instant invention: Type B CpG nucleic acids such as SEQ ID NO:1 include the earliest described CpG nucleic acids and characteristically activate B cells but do not induce or only weakly induce expression of IFN- α . Type B nucleic acids are described in U.S. Patents
10 6,194,388; 6,207,646; 6,214,806; 6,218,371; 6,239,116; and 6,339,068. Type A CpG nucleic acids, described in published international application PCT/US00/26527 (WO 01/22990), incorporate a CpG motif, include a hybrid phosphodiester/phosphorothioate backbone, and characteristically induce plasmacytoid dendritic cells to express large amounts of IFN- α but do not activate or only weakly activate B cells. Type C oligonucleotides incorporate a CpG,
15 include a chimeric backbone, include a GC-rich palindromic or nearly-palindromic region, and are capable of both activating B cells and inducing expression of IFN- α . These have been described, for example, in copending U.S. Pat. application Ser. No. 10/224,523, filed August 19, 2002. Exemplary sequences of A, B and C class nucleic acids are described in the afore-mentioned references, patents and patent applications, the entire contents of which are
20 hereby incorporated by reference herein.

In other embodiments of the invention, a non-CpG nucleic acid is used. A non-CpG nucleic acid is an immunostimulatory nucleic acid which either does not have a CpG motif in its sequence, or has a CpG motif which contains a methylated C residue. In some instances, the non-CpG nucleic acid may still be immunostimulatory by virtue of its having other
25 immunostimulatory motifs such as those described herein and known in the art. In one embodiment the non-CpG nucleic acid is a methylated CpG nucleic acid. In some instances the non-CpG nucleic acid is still immunostimulatory despite methylation of the C of the CpG motif, even without having another non-CpG immunostimulatory motif described herein and known in the art.

30 In one embodiment the non-CpG nucleic acid is a methylated CpG nucleic acid having a base sequence provided by 5'-TZGTZGTTTTGTZGTTTTGTZGTT-3' (SEQ ID NO:147), wherein Z represents 5-methylcytosine.

In one embodiment the non-CpG nucleic acid is a methylated CpG nucleic acid having a base sequence provided by 5'-TZGTZGZTGTZTZZGZTTZTTZTTGZZ-3' (SEQ ID NO:148), wherein Z represents 5-methylcytosine.

In one embodiment the non-CpG nucleic acid is a methylated CpG nucleic acid having
5 a base sequence provided by 5'-GZGTTTGZTZTTZTTZTTGZG-3' (SEQ ID NO:149), wherein Z represents 5-methylcytosine.

In one embodiment the non-CpG nucleic acid is a methylated CpG nucleic acid having a base sequence provided by 5'-GZZZAAGZTGGZATZZGTZA-3' (SEQ ID NO:150), wherein Z represents 5-methylcytosine.

10 Non-CpG nucleic acids include T-rich immunostimulatory nucleic acids. The T-rich immunostimulatory nucleic acids include those disclosed in published PCT patent application PCT/US00/26383 (WO 01/22972), the entire contents of which are incorporated herein by reference. In some embodiments, T-rich nucleic acids 24 bases in length are used. A T-rich nucleic acid is a nucleic acid which includes at least one poly T sequence and/or which has
15 a nucleotide composition of greater than 25% T nucleotide residues. A nucleic acid having a poly-T sequence includes at least four Ts in a row, such as 5'-TTTT-3'. In some embodiments the T-rich nucleic acid includes more than one poly T sequence. In important embodiments, the T-rich nucleic acid may have 2, 3, 4, or more poly T sequences, such as SEQ ID NO:1.

Non-CpG nucleic acids also include poly-G immunostimulatory nucleic acids. A
20 variety of references describe the immunostimulatory properties of poly-G nucleic acids. Pisetsky DS et al. (1993) *Mol Biol Reports* 18:217-221; Krieger M et al. (1994) *Ann Rev Biochem* 63:601-637; Macaya RF et al. (1993) *Proc Natl Acad Sci USA* 90:3745-3749; Wyatt JR et al. (1994) *Proc Natl Acad Sci USA* 91:1356-1360; Rando and Hogan, 1998, In *Applied Antisense Oligonucleotide Technology*, Krieg and Stein, eds., pp. 335-352; Kimura Y et al.
25 (1994) *J Biochem (Tokyo)* 116:991-994.

The immunostimulatory nucleic acids of the invention can also be those which do not possess CpG, methylated CpG, T-rich, or poly-G motifs.

Exemplary immunostimulatory nucleic acid sequences include but are not limited to those immunostimulatory sequences described and listed in U.S. Non-Provisional Pat.
30 Application No. 09/669,187, filed on September 25, 2000, and in corresponding published PCT patent application PCT/US00/26383 (WO 01/22972).

Immunoinhibitory nucleic acids have been described in Lenert P et al. (2001) *Antisense Nucleic Acid Drug Dev* 11:247-56 and in Stunz L et al. (2002) *Eur J Immunol*

32:1212-22. These inhibitory phosphorothioate ODN (S-ODN) differ from stimulatory S-ODN by having 2-3 G substitutions in the central motif. As inhibitory S-ODN did not directly interfere with the NF- κ B DNA binding but prevented CpG-induced NF- κ B nuclear translocation of p50, p65, and c-Rel and blocked p105, I κ B α , and I κ B β degradation, Lenert et al. suggested that the putative target of immunoinhibitory ODN would lie upstream of inhibitory kinase (IKK) activation. Stunz et al. reported that replacing GCGTT or ACGTT with GCGGG or ACGGG converted a stimulatory 15-mer ODN into an inhibitory ODN. All inhibitory ODN had three consecutive G, and a fourth G increased inhibitory activity, but a deazaguanosine substitution to prevent planar stacking did not affect activity. Inhibitory ODN blocked apoptosis protection and cell-cycle entry induced by stimulatory ODN, but not that induced by lipopolysaccharide, anti-CD40 or anti-IgM+IL-4. ODN-driven up-regulation of cyclin D(2), c-Myc, c-Fos, c-Jun and Bcl(XL) and down-regulation of cyclin kinase inhibitor p27(kip1) were all blocked by inhibitory ODN. Stunz et al. also reported that interference with uptake of stimulatory ODN did not account for the inhibitory effects of the immunoinhibitory nucleic acids.

In one embodiment the immunoinhibitory nucleic acid has a base sequence provided by 5'-TCCTGGCGGGGAAGT-3' (SEQ ID NO:151).

Immunoinhibitory nucleic acids have also been described in U.S. Pat. No. 6,194,388, issued to Krieg et al. The immunoinhibitory oligonucleotides disclosed by Krieg et al. are oligonucleotides with GCG trinucleotides at or near the ends of the oligonucleotide and are represented by the formula 5' GCGX_nGCG 3' in which X is a nucleotide and n is an integer between 0 and 50.

The nucleic acids used as either test or reference compounds can be double-stranded or single-stranded. They can be deoxyribonucleotide (DNA) or ribonucleotide (RNA) molecules. Generally, double-stranded molecules are more stable in vivo, while single-stranded molecules have increased immune activity. Thus in some the nucleic acid is single-stranded and in other embodiments the nucleic acid is double-stranded. In certain embodiments, while the nucleic acid is single-stranded, it is capable of forming secondary and tertiary structures (e.g., by folding back on itself, or by hybridizing with itself either throughout its entirety or at select segments along its length). Accordingly, while the primary structure of such a nucleic acid may be single-stranded, its higher order structures may be double- or triple-stranded.

For facilitating uptake into cells, the nucleic acids are preferably in the range of 6 to 100 bases in length. However, nucleic acids of any size equal to or greater than 6 nucleotides (even many kb long) are capable of inducing an immune response. Preferably the nucleic acid is in the range of between 8 and 100 and in some embodiments between 8 and 50 or 8 and 30 nucleotides in size.

The terms "nucleic acid" and "oligonucleotide" are used interchangeably to mean multiple nucleotides (i.e., molecules comprising a sugar (e.g., ribose or deoxyribose) linked to a phosphate group and to an exchangeable organic base, which is either a substituted pyrimidine (e.g., cytosine (C), thymine (T) or uracil (U)) or a substituted purine (e.g., adenine (A) or guanine (G)). As used herein, the terms "nucleic acid" and "oligonucleotide" refer to oligoribonucleotides as well as oligodeoxyribonucleotides. The terms "nucleic acid" and "oligonucleotide" shall also include polynucleosides (i.e., a polynucleotide minus the phosphate) and any other organic base containing polymer. Nucleic acid molecules can be obtained from existing nucleic acid sources (e.g., genomic or cDNA), but are preferably synthetic (e.g., produced by nucleic acid synthesis).

The terms "nucleic acid" and "oligonucleotide" also encompass nucleic acids or oligonucleotides with substitutions or modifications, such as in the bases and/or sugars. For example, they include nucleic acids having backbone sugars that are covalently attached to low molecular weight organic groups other than a hydroxyl group at the 2' position and other than a phosphate group or hydroxy group at the 5' position. Thus modified nucleic acids may include a 2'-O-alkylated ribose group. In addition, modified nucleic acids may include sugars such as arabinose or 2'-fluoroarabinose instead of ribose. Thus the nucleic acids may be heterogeneous in backbone composition thereby containing any possible combination of polymer units linked together such as peptide-nucleic acids (which have an amino acid backbone with nucleic acid bases). Other examples are described in more detail below.

The immunostimulatory and immunoinhibitory nucleic acids can encompass various chemical modifications and substitutions, in comparison to natural RNA and DNA, involving a phosphodiester internucleoside bridge, a β -D-ribose unit and/or a natural nucleoside base (adenine, guanine, cytosine, thymine, uracil). Examples of chemical modifications are known to the skilled person and are described, for example, in Uhlmann E et al. (1990) *Chem Rev* 90:543; "Protocols for Oligonucleotides and Analogs" Synthesis and Properties & Synthesis and Analytical Techniques, S. Agrawal, Ed, Humana Press, Totowa, USA 1993; Crooke ST et al. (1996) *Annu Rev Pharmacol Toxicol* 36:107-129; and Hunziker J et al. (1995) *Mod Synth*

Methods 7:331-417. An oligonucleotide according to the invention may have one or more modifications, wherein each modification is located at a particular phosphodiester internucleoside bridge and/or at a particular β -D-ribose unit and/or at a particular natural nucleoside base position in comparison to an oligonucleotide of the same sequence which is composed of natural DNA or RNA.

For example, the oligonucleotides may comprise one or more modifications and wherein each modification is independently selected from:

- a) the replacement of a phosphodiester internucleoside bridge located at the 3' and/or the 5' end of a nucleoside by a modified internucleoside bridge,
- b) the replacement of phosphodiester bridge located at the 3' and/or the 5' end of a nucleoside by a dephospho bridge,
- c) the replacement of a sugar phosphate unit from the sugar phosphate backbone by another unit,
- d) the replacement of a β -D-ribose unit by a modified sugar unit, and
- e) the replacement of a natural nucleoside base by a modified nucleoside base.

More detailed examples for the chemical modification of an oligonucleotide are as follows.

The oligonucleotides may include modified internucleotide linkages, such as those described in (a) or (b) above. These modified linkages may be partially resistant to degradation (e.g., are stabilized). A "stabilized oligonucleotide molecule" shall mean an oligonucleotide that is relatively resistant to *in vivo* degradation (e.g., via an exo- or endonuclease) resulting from such modifications. Oligonucleotides having phosphorothioate linkages, in some embodiments, may provide maximal activity and protect the oligonucleotide from degradation by intracellular exo- and endo-nucleases.

A phosphodiester internucleoside bridge located at the 3' and/or the 5' end of a nucleoside can be replaced by a modified internucleoside bridge, wherein the modified internucleoside bridge is for example selected from phosphorothioate, phosphorodithioate, NR^1R^2 -phosphoramidate, boranophosphate, α -hydroxybenzyl phosphonate, phosphate-(C_1 - C_{21})-O-alkyl ester, phosphate-[(C_6 - C_{12})aryl-(C_1 - C_{21})-O-alkyl]ester, (C_1 - C_8)alkylphosphonate and/or (C_6 - C_{12})arylphosphonate bridges, (C_7 - C_{12})- α -hydroxymethyl-aryl (e.g., disclosed in WO 95/01363), wherein (C_6 - C_{12})aryl, (C_6 - C_{20})aryl and (C_6 - C_{14})aryl are optionally substituted by halogen, alkyl, alkoxy, nitro, cyano, and where R^1 and R^2 are, independently of each other, hydrogen, (C_1 - C_{18})-alkyl, (C_6 - C_{20})-aryl, (C_6 - C_{14})-aryl-(C_1 - C_8)-alkyl, preferably hydrogen,

(C₁-C₈)-alkyl, preferably (C₁-C₄)-alkyl and/or methoxyethyl, or R¹ and R² form, together with the nitrogen atom carrying them, a 5-6-membered heterocyclic ring which can additionally contain a further heteroatom from the group O, S and N.

The replacement of a phosphodiester bridge located at the 3' and/or the 5' end of a nucleoside by a dephospho bridge (dephospho bridges are described, for example, in Uhlmann E and Peyman A in "Methods in Molecular Biology", Vol. 20, "Protocols for Oligonucleotides and Analogs", S. Agrawal, Ed., Humana Press, Totowa, 1993, Chapter 16, pp. 355 ff), wherein a dephospho bridge is for example selected from the dephospho bridges formacetal, 3'-thioformacetal, methylhydroxylamine, oxime, methylenedimethyl-hydrazo, dimethylenesulfone and/or silyl groups.

A sugar phosphate unit (i.e., a β -D-ribose and phosphodiester internucleoside bridge together forming a sugar phosphate unit) from the sugar phosphate backbone (i.e., a sugar phosphate backbone is composed of sugar phosphate units) can be replaced by another unit, wherein the other unit is for example suitable to build up a "morpholino-derivative" oligomer (as described, for example, in Stirchak EP et al. (1989) *Nucleic Acids Res* 17:6129-41), that is, e.g., the replacement by a morpholino-derivative unit; or to build up a polyamide nucleic acid ("PNA"; as described for example, in Nielsen PE et al. (1994) *Bioconjug Chem* 5:3-7), that is, e.g., the replacement by a PNA backbone unit, e.g., by 2-aminoethylglycine. The oligonucleotide may have other carbohydrate backbone modifications and replacements, such as peptide nucleic acids with phosphate groups (PHONA), locked nucleic acids (LNA), and oligonucleotides having backbone sections with alkyl linkers or amino linkers. The alkyl linker may be branched or unbranched, substituted or unsubstituted, and chirally pure or a racemic mixture.

A β -ribose unit or a β -D-2'-deoxyribose unit can be replaced by a modified sugar unit, wherein the modified sugar unit is for example selected from β -D-ribose, α -D-2'-deoxyribose, L-2'-deoxyribose, 2'-F-2'-deoxyribose, 2'-F-arabinose, 2'-O-(C₁-C₆)alkyl-ribose, preferably 2'-O-(C₁-C₆)alkyl-ribose is 2'-O-methylribose, 2'-O-(C₂-C₆)alkenyl-ribose, 2'-[O-(C₁-C₆)alkyl-O-(C₁-C₆)alkyl]-ribose, 2'-NH₂-2'-deoxyribose, β -D-xylo-furanose, α -arabinofuranose, 2,4-dideoxy- β -D-erythro-hexo-pyranose, and carbocyclic (described, for example, in Froehler J (1992) *Am Chem Soc* 114:8320) and/or open-chain sugar analogs (described, for example, in Vandendriessche et al. (1993) *Tetrahedron* 49:7223) and/or bicyclosugar analogs (described, for example, in Tarkov M et al. (1993) *Helv Chim Acta* 76:481).

In some embodiments the sugar is 2'-O-methylribose, particularly for one or both nucleotides linked by a phosphodiester or phosphodiester-like internucleoside linkage.

In some embodiments, the nucleic acids may be soft or semi-soft nucleic acids. A soft nucleic acid is an immunostimulatory nucleic acid having a partially stabilized backbone, in which phosphodiester or phosphodiester-like internucleotide linkages occur only within and immediately adjacent to at least one internal pyrimidine -purine dinucleotide (YZ). Preferably YZ is YG, a pyrimidine-guanosine (YG) dinucleotide. The at least one internal YZ dinucleotide itself has a phosphodiester or phosphodiester-like internucleotide linkage. A phosphodiester or phosphodiester-like internucleotide linkage occurring immediately adjacent to the at least one internal YZ dinucleotide can be 5', 3', or both 5' and 3' to the at least one internal YZ dinucleotide.

In particular, phosphodiester or phosphodiester-like internucleotide linkages involve "internal dinucleotides". An internal dinucleotide in general shall mean any pair of adjacent nucleotides connected by an internucleotide linkage, in which neither nucleotide in the pair of nucleotides is a terminal nucleotide, i.e., neither nucleotide in the pair of nucleotides is a nucleotide defining the 5' or 3' end of the nucleic acid. Thus a linear nucleic acid that is n nucleotides long has a total of $n-1$ dinucleotides and only $n-3$ internal dinucleotides. Each internucleotide linkage in an internal dinucleotide is an internal internucleotide linkage. Thus a linear nucleic acid that is n nucleotides long has a total of $n-1$ internucleotide linkages and only $n-3$ internal internucleotide linkages. The strategically placed phosphodiester or phosphodiester-like internucleotide linkages, therefore, refer to phosphodiester or phosphodiester-like internucleotide linkages positioned between any pair of nucleotides in the nucleic acid sequence. In some embodiments the phosphodiester or phosphodiester-like internucleotide linkages are not positioned between either pair of nucleotides closest to the 5' or 3' end.

Preferably a phosphodiester or phosphodiester-like internucleotide linkage occurring immediately adjacent to the at least one internal YZ dinucleotide is itself an internal internucleotide linkage. Thus for a sequence N_1 YZ N_2 , wherein N_1 and N_2 are each, independent of the other, any single nucleotide, the YZ dinucleotide has a phosphodiester or phosphodiester-like internucleotide linkage, and in addition (a) N_1 and Y are linked by a phosphodiester or phosphodiester-like internucleotide linkage when N_1 is an internal nucleotide, (b) Z and N_2 are linked by a phosphodiester or phosphodiester-like internucleotide linkage when N_2 is an internal nucleotide, or (c) N_1 and Y are linked by a phosphodiester or

phosphodiester-like internucleotide linkage when N_1 is an internal nucleotide and Z and N_2 are linked by a phosphodiester or phosphodiester-like internucleotide linkage when N_2 is an internal nucleotide.

Soft nucleic acids according to the instant invention are believed to be relatively
5 susceptible to nuclease cleavage compared to completely stabilized nucleic acids. Without meaning to be bound to a particular theory or mechanism, it is believed that soft nucleic acids of the invention are cleavable to fragments with reduced or no immunostimulatory activity relative to full-length soft nucleic acids. Incorporation of at least one nuclease-sensitive internucleotide linkage, particularly near the middle of the nucleic acid, is believed to provide
10 an "off switch" which alters the pharmacokinetics of the nucleic acid so as to reduce the duration of maximal immunostimulatory activity of the nucleic acid. This can be of particular value in tissues and in clinical applications in which it is desirable to avoid injury related to chronic local inflammation or immunostimulation, e.g., the kidney.

A semi-soft nucleic acid is an immunostimulatory nucleic acid having a partially
15 stabilized backbone, in which phosphodiester or phosphodiester-like internucleotide linkages occur only within at least one internal pyrimidine-purine (YZ) dinucleotide. Semi-soft nucleic acids generally possess increased immunostimulatory potency relative to corresponding fully stabilized immunostimulatory nucleic acids. Due to the greater potency of semi-soft nucleic acids, semi-soft nucleic acids may be used, in some instances, at lower
20 effective concentrations and have lower effective doses than conventional fully stabilized immunostimulatory nucleic acids in order to achieve a desired biological effect.

It is believed that the foregoing properties of semi-soft nucleic acids generally increase with increasing "dose" of phosphodiester or phosphodiester-like internucleotide linkages involving internal YZ dinucleotides. Thus it is believed, for example, that generally for a
25 given nucleic acid sequence with five internal YZ dinucleotides, a nucleic acid with five internal phosphodiester or phosphodiester-like YZ internucleotide linkages is more immunostimulatory than a nucleic acid with four internal phosphodiester or phosphodiester-like YG internucleotide linkages, which in turn is more immunostimulatory than a nucleic acid with three internal phosphodiester or phosphodiester-like YZ internucleotide linkages,
30 which in turn is more immunostimulatory than a nucleic acid with two internal phosphodiester or phosphodiester-like YZ internucleotide linkages, which in turn is more immunostimulatory than a nucleic acid with one internal phosphodiester or phosphodiester-like YZ internucleotide linkage. Importantly, inclusion of even one internal phosphodiester or

phosphodiester-like YZ internucleotide linkage is believed to be advantageous over no internal phosphodiester or phosphodiester-like YZ internucleotide linkage. In addition to the number of phosphodiester or phosphodiester-like internucleotide linkages, the position along the length of the nucleic acid can also affect potency.

5 The soft and semi-soft nucleic acids will generally include, in addition to the phosphodiester or phosphodiester-like internucleotide linkages at preferred internal positions, 5' and 3' ends that are resistant to degradation. Such degradation-resistant ends can involve any suitable modification that results in an increased resistance against exonuclease digestion over corresponding unmodified ends. For instance, the 5' and 3' ends can be stabilized by the
10 inclusion thereof at least one phosphate modification of the backbone. In a preferred embodiment, the at least one phosphate modification of the backbone at each end is independently a phosphorothioate, phosphorodithioate, methylphosphonate, or methylphosphorothioate internucleotide linkage. In another embodiment, the degradation-resistant end includes one or more nucleotide units connected by peptide or amide linkages at
15 the 3' end.

 A phosphodiester internucleotide linkage is the type of linkage characteristic of nucleic acids found in nature. The phosphodiester internucleotide linkage includes a phosphorus atom flanked by two bridging oxygen atoms and bound also by two additional oxygen atoms, one charged and the other uncharged. Phosphodiester internucleotide linkage
20 is particularly preferred when it is important to reduce the tissue half-life of the nucleic acid.

 A phosphodiester-like internucleotide linkage is a phosphorus-containing bridging group that is chemically and/or diastereomerically similar to phosphodiester. Measures of similarity to phosphodiester include susceptibility to nuclease digestion and ability to activate RNase H. Thus for example phosphodiester, but not phosphorothioate, nucleic acids are
25 susceptible to nuclease digestion, while both phosphodiester and phosphorothioate nucleic acids activate RNase H. In a preferred embodiment the phosphodiester-like internucleotide linkage is boranophosphate (or equivalently, boranophosphonate) linkage. U.S. Patent No. 5,177,198; U.S. Patent No. 5,859,231; U.S. Patent No. 6,160,109; U.S. Patent No. 6,207,819; Sergueev et al., (1998) *J Am Chem Soc* 120:9417-27. In another preferred embodiment the
30 phosphodiester-like internucleotide linkage is diastereomerically pure Rp phosphorothioate. It is believed that diastereomerically pure Rp phosphorothioate is more susceptible to nuclease digestion and is better at activating RNase H than mixed or diastereomerically pure Sp phosphorothioate. Stereoisomers of CpG nucleic acids are the subject of co-pending U.S.

patent application 09/361,575 filed July 27, 1999, and published PCT application PCT/US99/17100 (WO 00/06588). It is to be noted that for purposes of the instant invention, the term "phosphodiester-like internucleotide linkage" specifically excludes phosphorodithioate and methylphosphonate internucleotide linkages.

5 As described above the soft and semi-soft nucleic acids of the invention may have phosphodiester like linkages between C and G. One example of a phosphodiester-like linkage is a phosphorothioate linkage in an R_p conformation. Nucleic acid p-chirality can have apparently opposite effects on the immune activity of a CpG nucleic acid, depending upon the time point at which activity is measured. At an early time point of 40 minutes, the R_p but not
10 the S_p stereoisomer of phosphorothioate CpG nucleic acid induces JNK phosphorylation in mouse spleen cells. In contrast, when assayed at a late time point of 44 hr, the S_p but not the R_p stereoisomer is active in stimulating spleen cell proliferation. This difference in the kinetics and bioactivity of the R_p and S_p stereoisomers does not result from any difference in cell uptake, but rather most likely is due to two opposing biologic roles of the p-chirality.
15 First, the enhanced activity of the R_p stereoisomer compared to the S_p for stimulating immune cells at early time points indicates that the R_p may be more effective at interacting with the CpG receptor, TLR9, or inducing the downstream signaling pathways. On the other hand, the faster degradation of the R_p PS-nucleic acids compared to the S_p results in a much shorter duration of signaling, so that the S_p PS-nucleic acids appear to be more biologically
20 active when tested at later time points.

A surprisingly strong effect is achieved by the p-chirality at the CpG dinucleotide itself. In comparison to a stereo-random CpG nucleic acid the congener in which the single CpG dinucleotide was linked in R_p was slightly more active, while the congener containing an S_p linkage was nearly inactive for inducing spleen cell proliferation.

25 Nucleic acids also include substituted purines and pyrimidines such as C-5 propyne pyrimidine and 7-deaza-7-substituted purine modified bases. Wagner RW et al. (1996) *Nat Biotechnol* 14:840-4. Purines and pyrimidines include but are not limited to adenine, cytosine, guanine, and thymine, and other naturally and non-naturally occurring nucleobases, substituted and unsubstituted aromatic moieties.

30 A modified base is any base which is chemically distinct from the naturally occurring bases typically found in DNA and RNA such as T, C, G, A, and U, but which share basic chemical structures with these naturally occurring bases. The modified nucleoside base may be, for example, selected from hypoxanthine, uracil, dihydrouracil, pseudouracil, 2-thiouracil,

4-thiouracil, 5-aminouracil, 5-(C₁-C₆)-alkyluracil, 5-(C₂-C₆)-alkenyluracil, 5-(C₂-C₆)-alkynyluracil, 5-(hydroxymethyl)uracil, 5-chlorouracil, 5-fluorouracil, 5-bromouracil, 5-hydroxycytosine, 5-(C₁-C₆)-alkylcytosine, 5-(C₂-C₆)-alkenylcytosine, 5-(C₂-C₆)-alkynylcytosine, 5-chlorocytosine, 5-fluorocytosine, 5-bromocytosine, N²-dimethylguanine, 5
2,4-diamino-purine, 8-azapurine, a substituted 7-deazapurine, preferably 7-deaza-7-substituted and/or 7-deaza-8-substituted purine, 5-hydroxymethylcytosine, N4-alkylcytosine, e.g., N4-ethylcytosine, 5-hydroxydeoxycytidine, 5-hydroxymethyldeoxycytidine, N4-alkyldeoxycytidine, e.g., N4-ethyldeoxycytidine, 6-thiodeoxyguanosine, and deoxyribonucleosides of nitropyrrole, C5-propynylpyrimidine, and
10 diaminopurine e.g., 2,6-diaminopurine, inosine, 5-methylcytosine, 2-aminopurine, 2-amino-6-chloropurine, hypoxanthine or other modifications of a natural nucleoside bases. This list is meant to be exemplary and is not to be interpreted to be limiting.

Modified cytosines include but are not limited to 5-substituted cytosines (e.g., 5-methyl-cytosine, 5-fluoro-cytosine, 5-chloro-cytosine, 5-bromo-cytosine, 5-iodo-cytosine, 5-
15 hydroxy-cytosine, 5-hydroxymethyl-cytosine, 5-difluoromethyl-cytosine, and unsubstituted or substituted 5-alkynyl-cytosine), 6-substituted cytosines, N4-substituted cytosines (e.g., N4-ethyl-cytosine), 5-aza-cytosine, 2-mercapto-cytosine, isocytosine, pseudo-isocytosine, cytosine analogs with condensed ring systems (e.g., N,N'-propylene cytosine or phenoxazine), and uracil and its derivatives (e.g., 5-fluoro-uracil, 5-bromo-uracil, 5-
20 bromovinyl-uracil, 4-thio-uracil, 5-hydroxy-uracil, 5-propynyl-uracil). In another embodiment, the cytosine base is substituted by a universal base (e.g., 3-nitropyrrole, P-base), an aromatic ring system (e.g., fluorobenzene or difluorobenzene) or a hydrogen atom (dSpacer).

Modified guanines include but are not limited to 7-deazaguanine, 7-deaza-7-substituted guanine (such as 7-deaza-7-(C₂-C₆)alkynylguanine),
25 7-deaza-8-substituted guanine, hypoxanthine, N2-substituted guanines (e.g., N2-methyl-guanine), 5-amino-3-methyl-3H,6H-thiazolo[4,5-d]pyrimidine-2,7-dione, 2,6-diaminopurine, 2-aminopurine, purine, indole, adenine, substituted adenines (e.g., N6-methyl-adenine, 8-oxo-adenine) 8-substituted guanine (e.g., 8-hydroxyguanine and 8-bromoguanine), and
30 6-thioguanine. In another embodiment, the guanine base is substituted by a universal base (e.g., 4-methyl-indole, 5-nitro-indole, and K-base), an aromatic ring system (e.g., benzimidazole or dichloro-benzimidazole, 1-methyl-1H-[1,2,4]triazole-3-carboxylic acid amide) or a hydrogen atom (dSpacer).

For use in the instant invention, the oligonucleotide reference compounds and test compounds can be synthesized *de novo* using any of a number of procedures well known in the art, for example, the β -cyanoethyl phosphoramidite method (Beaucage SL et al. (1981) *Tetrahedron Lett* 22:1859), or the nucleoside H-phosphonate method (Garegg et al. (1986) *Tetrahedron Lett* 27:4051-4; Froehler BC et al. (1986) *Nucleic Acids Res* 14:5399-407; Garegg et al (1986) *Tetrahedron Lett* 27:4055-8; Gaffney et al. (1988) *Tetrahedron Lett* 29:2619-22). These chemistries can be performed by a variety of automated nucleic acid synthesizers available in the market. These oligonucleotides are referred to as synthetic oligonucleotides. An isolated oligonucleotide generally refers to an oligonucleotide which is separated from components which it is normally associated with in nature. As an example, an isolated oligonucleotide may be one which is separated from a cell, from a nucleus, from mitochondria or from chromatin.

Modified backbones such as phosphorothioates can be synthesized using automated techniques employing either phosphoramidate or H-phosphonate chemistries. Aryl- and alkyl-phosphonates can be made, e.g., as described in U.S. Pat. No. 4,469,863; and alkylphosphotriesters (in which the charged oxygen moiety is alkylated as described in U.S. Pat. No. 5,023,243 and European Pat. No. 092,574) can be prepared by automated solid phase synthesis using commercially available reagents. Methods for making other DNA backbone modifications and substitutions have been described (e.g., Uhlmann E et al. (1990) *Chem Rev* 90:544; Goodchild J (1990) *Bioconjugate Chem* 1:165).

TLR expression

The cell lines can be used in their native state without any modification. For example, in the case of the RPMI 8226 cell line, it can be used to identify compounds that signal through at least TLR9 and/or TLR7. In other instances, however, the cell line can be modified to express a TLR that it does not naturally express. In still other instances, the cell to be used in the screening method may express one or more endogenous TLR and yet still be manipulated to express an additional TLR different from those it endogenously expresses. The cell may also be manipulated in order to increase or decrease the level of TLR that it endogenously expresses. The cells may be stably or transiently transfected.

A cell that does not naturally express a protein or polypeptide, but is genetically manipulated to do so is referred to as ectopically expressing the protein or polypeptide.

The basic screening method remains the same regardless of which TLR is expressed by the cell. However, the reference compound and the readout may vary depending upon the TLR(s) expressed. In the most simple aspect, the screening method is used to identify a compound that signals through a TLR such as for example TLR9. In this case, the positive reference compound may be an immunostimulatory compound already known to act through TLR9 (e.g., CpG nucleic acid).

The methods of the invention involve, in part, contacting a functional TLR with a test composition. A functional TLR is a full-length TLR protein or a fragment thereof capable of inducing or inhibiting a signal in response to interaction with its ligand. Generally the functional TLR will include at least a TLR ligand-binding fragment of the extracellular domain of the full-length TLR and at least a fragment of a TIR domain capable of interacting with another Toll homology domain-containing polypeptide, e.g., MyD88. In various embodiments the functional TLR is a full-length TLR selected from TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9, and TLR10.

To date, there are eleven TLRs known. Nucleic acid and amino acid sequences for ten currently known human TLRs are available from public databases such as GenBank. Similarly, nucleic acid and amino acid sequences for various TLRs from numerous non-human species are also available from public databases including GenBank. For example, nucleic acid and amino acid sequences for human TLR9 (hTLR9) can be found as GenBank accession numbers AF245704 (coding region spanning nucleotides 145-3243) (SEQ ID NO: 60) and AAF78037 (SEQ ID NO: 62), respectively. Nucleic acid and amino acid sequences for murine TLR9 (mTLR9) can be found as GenBank accession numbers AF348140 (coding region spanning nucleotides 40-3138) (SEQ ID NO: 68) and AAK29625 (SEQ ID NO: 72), respectively.

Nucleic acid and amino acid sequences for human TLR8 (hTLR8) can be found as GenBank accession numbers AF245703 (coding region spanning nucleotides 49-3174) (SEQ ID NO: 46) and AAF78036 (SEQ ID NO: 50), respectively. Nucleic acid and amino acid sequences for murine TLR8 (mTLR8) can be found as GenBank accession numbers AY035890 (coding region spanning nucleotides 59-3157) (SEQ ID NO: 55) and AAK62677 (SEQ ID NO: 57), respectively.

Nucleic acid and amino acid sequences for human TLR7 (hTLR7) can be found as GenBank accession numbers AF240467 (coding region spanning nucleotides 135-3285) (SEQ ID NO: 31) and AAF60188 (SEQ ID NO: 34), respectively. Nucleic acid and amino acid

sequences for murine TLR7 (mTLR7) can be found as GenBank accession numbers AY035889 (coding region spanning nucleotides 49-3201) (SEQ ID NO: 38) and AAK62676 (SEQ ID NO: 41), respectively.

Nucleic acid and amino acid sequences for human TLR3 (hTLR3) can be found as GenBank accession numbers NM_003265 (coding region spanning nucleotides 102-2816) (SEQ ID NO: 7) and NP_003256 (SEQ ID NO: 8), respectively. Nucleic acid and amino acid sequences for murine TLR3 (hTLR3) can be found as GenBank accession numbers AF355152 (coding region spanning nucleotides 44-2761) (SEQ ID NO: 9) and AAK26117 (SEQ ID NO: 10), respectively.

Nucleic acid and amino acid sequences for human TLR1 (hTLR1) can be found as GenBank accession numbers NM_003263 and NP_003254, respectively. Nucleic acid and amino acid sequences for murine TLR1 (mTLR1) can be found as GenBank accession numbers NM_030682 and NP_109607, respectively.

The functional TLR also is not limited to native TLR polypeptides. As used herein, a native TLR is one that is naturally occurring. The TLR may be a non-native (or non-naturally occurring TLR). An example is a chimeric TLR having an extracellular domain and the cytoplasmic domain derived from TLRs from different species. Such chimeric TLR polypeptides can include, for example, a human TLR extracellular domain and a murine TLR cytoplasmic domain. In alternative embodiments, such chimeric TLR polypeptides can include chimerae created with different TLR splice variants or allotypes.

TLR Signaling Pathways

The screening methods provided by the invention measure TLR signaling activity. TLR signaling activity is activity that results from interaction of a TLR with a TLR ligand. TLR signaling can be measured in a number of ways including but not limited to interaction between a TLR and a protein or factor (such as an adaptor protein), interaction between downstream proteins or factors (such as an adaptor protein) with each other, activation of nuclear factors such as transcription factors or transcription complexes, up- or down-regulation of genes, phosphorylation or dephosphorylation of proteins or factors in the signaling cascade, expression, production and/or secretion of cytokines and/or chemokines, changes in cell cycle status, up- or down-regulation of cell surface marker expression, and the like. Those of ordinary skill in the art are familiar with assays for measuring these latter

events including but not limited to gel shift assays, immunoprecipitations, phosphorylation status analysis of proteins, Northern analysis, RT-PCR analysis, etc.

The following is an exemplary TLR signaling pathway or cascade. It is to be understood that this is meant to be illustrative and that different factors may be involved in the signaling of particular TLR. One TLR signaling pathway is known to use the cytoplasmic Toll/IL-1 receptor (TIR) homology domain, present in all TLRs. This domain interacts (e.g., binds to) and thereby transduces a signal to a similar domain on an adapter protein (e.g., MyD88). This type of interaction is referred to as a like:like interaction of TIR domains. This interaction is followed by an another interaction between the adapter protein and a kinase, through their respective "death domains". In the case of at least TLR4 signaling, the kinase then interacts with tumor necrosis factor (TNF) receptor-associated factor-6 (TRAF6). Medzhitov R et al., *Mol Cell* 2:253 (1998); Kopp EB et al., *Curr Opin Immunol* 11:15 (1999). After TRAF6, two sequential kinase activation steps lead to phosphorylation of the inhibitory protein I kappa B and its dissociation from NF- κ B. The first kinase is a mitogen-activated kinase kinase kinase (MAPKKK) known as NIK, for NF- κ B-inducing kinase. The target of this kinase is another kinase made up of two chains, called I kappa B kinase α (IKK α) and I kappa B kinase β (IKK β), that together form a heterodimer of IKK α :IKK β , which phosphorylates I kappa B. NF- κ B translocates to the nucleus to activate genes with kappa B binding sites in their promoters and enhancers such as the genes encoding IL-6, IL-8, the p40 subunit of IL-12, and the costimulatory molecule CD86. The signaling mechanisms of TLRs are not limited to this pathway; other signaling pathways exist and can be used in the screening readouts of the methods provided herein.

The screening assays employ a number of readouts (or parameters). The readouts can be native readouts. A native readout is one that does not rely on introduction of a reporter construct into the cell of interest. The readouts can be artificial. An artificial readout is one that relies on introduction of a reporter construct into the cell of interest. Examples of both are provided herein. In still other embodiments, a given assay may measure one or more native readouts and one or more artificial readouts. Each readout whether native or artificial is related to signaling pathways that ensue after TLR engagement with a ligand.

Each cell line described herein will be associated with a particular set of native readouts which the invention seeks to determine in the screening assays provided. As an example, the response of the RPMI 8226 cell line to an immunomodulatory molecule can be assessed in terms of native readouts such as CD71 expression, CD86 expression, HLA-DR

expression, IL-8 expression, IL-8 production, IL-8 secretion, IL-10 expression, IL-10 production, IL-10 secretion, IP-10 expression, IP-10 production, IP-10 secretion, TNF- α expression, TNF- α production and TNF- α secretion. RAMOS response can be assessed, inter alia, by CD80 cell surface expression. Raji response can be assessed, inter alia, by IL-6 secretion.

As described in greater detail herein, the cell line can be used in an unmodified form. In one respect, an unmodified cell line will naturally respond to a TLR ligand through a native readout system. For example, an RPMI 8226 cell exposed to an immunostimulatory TLR ligand may increase expression of IP-10 from the native gene locus. Alternatively, the cell line may be modified to contain a reporter construct that acts as a surrogate for the IP-10 gene locus. For example, the reporter construct may contain the TLR responsive promoter elements that are naturally found in the native IP-10 locus operably linked to a reporter coding sequence that encodes a gene product that is detectable and quantifiable. The structure and variability of suitable reporter constructs will be discussed in greater detail herein.

Readouts typically include the induction of a gene under control of a specific promoter such as a NF- κ B promoter. The gene under the control of the NF- κ B promoter can be a gene which naturally includes an NF- κ B promoter or it can be a gene in a construct in which an NF- κ B promoter has been inserted. Endogenous genes and transfected constructs which include the NF- κ B promoter include but are not limited to IL-8, IL-12 p40, NF- κ B-luc, IL-12 p40-luc, and TNF-luc.

Increases in cytokine levels can result from increased production, increased stability, increased secretion, or any combination of the forgoing, of the cytokine in response to the TLR-mediated signaling. Cytokines generally include, without limitation, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-10, IL-11, IL-12, IL-13, IL-15, IL-18, IFN- α , IFN- β , IFN- γ , TNF- α , GM-CSF, G-CSF, M-CSF. Th1 cytokines include but are not limited to IL-2, IFN- γ , and IL-12. Th2 cytokines include but are not limited to IL-4, IL-5, and IL-10.

Increases in chemokine levels can result from increased production, increased stability, increased secretion, or any combination of the forgoing, of the chemokine in response to the TLR-mediated signaling. Chemokines of particular significance in the invention include but are not limited to CCL5 (RANTES), CXCL9 (Mig), CXCL10 (IP-10), CXCL11 (I-TAC), IL-8, and MCP-1.

TLR signaling activity can also be measured by phosphorylation, such as total cellular phosphorylation or phosphorylation of specific factors such as but not limited to IRAK, ERK, MyD88, TRAF6, p38, NF- κ B subunits, c-Jun and c-Fos.

TLR signaling activity can be measured by changes in gene expression. The
5 expression of CD71, CD86, CD80, CD69, CD54, HLA-DR, HLA class I, IL-6, IL-8, IL-10, IP-9, IP-10, IFN- α , TNF- α , and the like can be assessed as a measure of TLR signaling activity. Gene expression analysis may be performed using microarray techniques.

TLR signaling activity can also be measured by cell proliferation status or changes thereto.

10 TLR signaling activity can also be measured by cell surface marker expression such as the cell surface expression of markers such as but not limited to CD71, CD86, HLA-DR, CD80, HLA class I, CD54 and CD69.

TLR signaling activity can also be measured by antibody secretion such as but not limited to IgM secretion.

15 Reporter and Expression Constructs

The cells can be manipulated by the introduction of expression and/or reporter constructs. The expression constructs preferably comprise a TLR coding sequence, as described above. The reporter constructs can be used as surrogate measures of native TLR
20 signaling activity. These reporter constructs are intended to substitute for the "native" readouts capable with the cell line. In order to act as substitutes, the reporter constructs include a promoter element derived from a gene known to be modulated following TLR engagement with a TLR ligand. The reporter construct further includes a coding sequence linked to the promoter. The coding sequence is usually that of a reporter (i.e., a protein that is
25 detectable or quantifiable).

The reporter construct generally includes a promoter, a coding sequence and a polyadenylation signal. These nucleic acids shall include, as necessary, 5' non-transcribing and 5' non-translating sequences involved with the initiation of transcription and translation, respectively, such as a TATA box, capping sequence, CAAT sequence, in addition to
30 promoter elements that are responsive to TLR signaling. The nucleic acid constructs may optionally include enhancer sequences or upstream activator sequences as desired.

The promoter in the reporter construct will include a TLR responsive promoter element, and will therefore be regarded as a TLR responsive promoter. As used herein, a

TLR responsive promoter is a promoter having an activity that is modulated (i.e., either activated or inhibited) by signaling through a TLR (e.g., by TLR interaction with its ligand). In order to be modulated by TLR signaling, the promoter contains sites that are bound by transcription factors modulated by TLR signaling. The factors may be activated or inhibited by TLR signaling. Activation of the transcription factor includes increases in the activity of the transcription factor per se, increases in its ability to interact with other factors or with DNA that serve to increase its activity, and increases in its transcription and translation (i.e., increased mRNA and protein levels of the transcription factor). Conversely, inhibition of the transcription factor includes decreases in the activity of the transcription factor per se, decreases in its ability to interact with other factors or with DNA that serve to decrease its activity, and decreases in its transcription and translation (i.e., decreased mRNA and protein levels of the transcription factor). The effect on the transcription factor is usually the downstream result of other interactions in the signaling pathway. The expression of coding sequences linked to such promoters will therefore be modulated by TLR signaling events, and it is the level of expression of these coding sequences that can be used as a readout of TLR signaling in the screening methods provided herein.

The TLR responsive promoter may comprise a transcription factor binding site selected from the group consisting of a NF- κ B binding site, an AP-1 binding site, a CRE, a SRE, an interferon-stimulated response element (ISRE), a GAS, an ATF2 binding site, an IRF3 binding site, an IRF7 binding site, an NFAT binding site, a p53 binding site, an SRF binding site, and a TARE, among others. These binding sites and their sequences are known in the art. Below is an exemplary list of these sequences.

W = A or T, R = A or G, Y = C or T

NF- κ B Binding site:

Consensus p50 subunit
5' GGGGATYCCC 3' (SEQ ID NO:90)

Consensus p65 subunit
5' GGRNTTTC 3' (SEQ ID NO:91)

Example of p65 subunit binding site
5' AGT TGA GGG GAC TTT CCC AGG C 3' (SEQ ID NO:92)

CREB Binding site:

5'AGA GAT TGC CTG ACG TCA GAG AGC TAG 3' (SEQ ID NO:93)

AP-1 Binding site:

5'- CGC TTG ATG AGT CAG CCG GAA -3' (SEQ ID NO:94)

5'- CGC ATG AGT CAG ACA -3' (SEQ ID NO:95)

5 ISRE :

5'- TGCAGAAAGTGAAACTGAGG-3' (SEQ ID NO:96)

5'- AGAACGAAACA-3' (SEQ ID NO:97)

5'- GAGAAGTGAAAGTGG-3' (SEQ ID NO:98)

5'- TAAGAACATGAAACTGAA-3' (SEQ ID NO:99)

10 5'- ATGAAACTGAAAGTA-3' (SEQ ID NO:100)

5'- TGAAAACCGAAAGCGC-3' (SEQ ID NO:101)

5'- AGAAATGGAAAGT-3' (SEQ ID NO:102)

SRE

15 5'- TCACCCAC-3' (SEQ ID NO:103)

5'- CTCACCCAC-3' (SEQ ID NO:104)

5'- GCCACCCTAC-3' (SEQ ID NO:105)

NFAT:

20 5'- TATGAAACAGTTTTTCC -3' (SEQ ID NO:106)

5'- AGGAAACTC -3' (SEQ ID NO:107)

5'- ARGARATTCC -3' (SEQ ID NO:108)

5'- CCAGTTGAGCCAGAGA -3' (SEQ ID NO:109)

25 GAS:

5'- CTTTCAGTTTCATATTACTCTAAATCCATT -3' (SEQ ID NO:110)

p53 Binding Site :

30 p53 Consensus site:

5'- RRRCWWGYYY -3' (SEQ ID NO:111)

Examples of p53 binding sites:

5'- AGGCATGCCT -3' (SEQ ID NO:112)

35 5'- GGGCTTGCCC -3' (SEQ ID NO:113)

5'- GGGCTTGCTT -3' (SEQ ID NO:114)

5'- GCCTGGACTTGCC -3' (SEQ ID NO:115)

5'- GGACATGCCCCGGGCATGTCC -3' (SEQ ID NO:116)

5'- GTAGCATTAGCCCAGACATGTCC -3' (SEQ ID NO:117)

40

TARE (TNF- α response element):

e.g. from the COL1A1 promoter

5'GAGGTATGCAGACAAGAGTCAGAGTTTCCCCTTGAA 3' (SEQ ID

NO:118)

45

SRF

5'- CCWWWWWWGG -3' (SEQ ID NO:119)

5'- CCAAATAAGGC -3' (SEQ ID NO:120)

The TLR responsive promoter element can be derived from the promoter of a naturally occurring (i.e., an endogenous) gene that is activated or inhibited by TLR signaling (such as the IL-6 gene, the IL-8 gene, the IL-10 gene, the IL-12 p40 gene, the IP-9 gene, the IP-10 gene, the type 1 IFN gene, the IFN- α 4 gene, the IFN- β gene, the TNF- α gene, the TNF- β gene, the RANTES gene, the ITAC gene, the IGFBP4 gene, the CD54 gene, the CD69 gene, the CD71 gene, the CD80 gene, the CD86 gene, the HLA-DR gene, the HLA class I gene, and the like). The afore-mentioned genes are genes that are known to be activated in response to TLR interaction with its ligand.

Suitable promoter regions are described in the Examples. Briefly, the upstream (5') – 620 to +50 promoter region of IFN- α 4 or the upstream (5') –140 to +9 promoter region of IFN- α 1 can be used. In one embodiment, the IFN- α 4 sequence is cloned into the *Sma*I site of the pGL3-Basic Vector (Promega) resulting in an expression vector that includes a luciferase gene under the control of the upstream (5') promoter region of IFN- α 4.

The promoter can also be the upstream (5') –280 to +20 promoter region of IFN- β .

The promoter can also be the upstream (5') –397 to +5 promoter region of RANTES. In one embodiment, the RANTES promoter sequence is cloned into the *Nhe*I site (filled in with Klenow) of the pGL3-Basic Vector (Promega) resulting in an expression vector that includes a luciferase gene under the control of the upstream (5') –397 to +5 promoter region of RANTES.

The promoter can also be the upstream truncated (-250 to +30) and full length (-860 to +30) promoter regions derived from human IL-12 p40 genomic DNA. In one embodiment, the truncated IL-12 p40 promoter was cloned as a *Kpn*I-*Xho*I insert into p β gal-Basic (Promega) resulting in an expression vector that includes a β gal gene under the control of the upstream (5') –250 to +30 promoter region of human IL-12 p40. In another embodiment, the full length IL-12 p40 promoter was cloned as a *Kpn*I-*Xho*I insert into p β gal-Basic (Promega) resulting in an expression vector that includes a β gal gene under the control of the upstream (5') –751 to +30 promoter region of human IL-12 p40. In another embodiment, the truncated –250 to +30 promoter region of human IL-12 p40 was cloned into the pGL3-Basic Vector (Promega) resulting in an expression vector that includes a luciferase gene under the control of the upstream (5') –250 to +30 promoter region of human IL-12 p40. In yet another embodiment, the full length IL-12 p40 promoter of human IL-12 p40 was cloned into the

pGL3-Basic Vector (Promega) resulting in an expression vector that includes a luciferase gene under the control of the upstream (5') -751 to +30 promoter region of human IL-12 p40.

The promoter can also be the upstream (5') -288 to +7 promoter region derived from human IL-6 genomic DNA. The promoter can also be derived from the full-length promoter
5 region of the IL-6 gene from -1174 to +7 (Accession No M22111, SEQ ID NO:129).

The promoter can also be the upstream (5') -734 to +44 or the upstream (5') -162 to +44 promoter region derived from human IL-8 genomic DNA. Mukaida N et al. (1989) *J Immunol* 143:1366-71.

The promoter can also be derived from the -615 to +30 promoter region of human
10 TNF- α .

The promoter can also be derived from a promoter region of human TNF- β .

The promoter can also be derived from the -875 to +97 promoter region of human IP-
10.

The promoter can also be derived from the -219 to +114 promoter region of human
15 CXCL11 (IP9). The promoter can also be derived from the full length (-934 to +114) promoter region of human CXCL11 (IP9).

The promoter can also be derived from the -289 to +217 promoter region of human IGFBP4 (Insulin growth factor binding protein 4). The promoter can also be derived from the full length (-836 to +217) promoter region of human IGFBP4.

20 The promoter response element generally will be present in multiple copies, e.g., as tandem repeats. For example, in one reporter construct, coding sequence for luciferase is under control of an upstream 6X tandem repeat of NF- κ B response element. In another example, an ISRE-luciferase reporter construct useful in the invention is available from Stratagene (catalog no. 219092) and includes a 5x ISRE tandem repeat joined to a TATA box
25 upstream of a luciferase reporter gene.

The reporter construct coding sequence is preferably any nucleotide sequence that codes for a protein capable of detection or quantification. The protein can be an enzyme (e.g., luciferase, alkaline phosphatase, β -galactosidase, chloramphenicol acetyltransferase (CAT), secreted alkaline phosphatase, etc.), a bioluminescence marker (e.g., green fluorescent protein
30 (GFP, U.S. Pat. No. 5,491,084), etc.), blue fluorescent protein (BFP, e.g., U.S. Pat. No. 6,486,382), etc.), a surface-expressed molecule (e.g., CD25, CD80, CD86), a secreted molecule (e.g., IL-1, IL-6, IL-8, IL-12 p40, TNF- α), a hapten or antigen, and other detectable protein products known to those of skill in the art. For assays relying on enzyme activity

readout, substrate can be supplied as part of the assay, and detection can involve measurement of chemiluminescence, fluorescence, color development, incorporation of radioactive label, drug resistance, or other marker of enzyme activity. For assays relying on surface expression of a molecule, detection can be accomplished using flow cytometry (FACS) analysis or functional assays. Secreted molecules can be assayed using enzyme-linked immunosorbent assay (ELISA) or bioassays. Many of these and other suitable readout systems are well known in the art and are commercially available. Preferably, the coding sequence encodes a protein having a level or an activity that is quantifiable, preferably with a wide linear range.

The expression construct coding sequence is preferably a TLR coding sequence derived from the sequences listed herein. Preferably, the expression construct promoter is a constitutive promoter, although in some embodiments it may be inducible. Those of ordinary skill in the art are familiar with such promoters.

As used herein, a coding sequence and the regulatory sequences (such as promoters) are said to be operably linked when they are covalently linked in such a way as to place the expression or transcription and/or translation of the coding sequence under the influence or control of the regulatory sequence. Two DNA sequences are said to be operably linked if induction of a promoter in the 5' regulatory sequence results in the transcription of the coding sequence and if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region to direct the transcription of the coding sequence, or (3) interfere with the ability of the corresponding RNA transcript to be translated into a protein. Thus, a regulatory sequence would be operably linked to a coding sequence if the gene expression sequence were capable of effecting transcription of that coding sequence such that the resulting transcript is translated into the desired protein or polypeptide.

Methods for nucleic acid introduction into cells are known in the art.

The nucleic acid may be delivered to the cells alone or in association with a vector. In its broadest sense, a vector is any vehicle capable of facilitating the transfer of the nucleic acid to the cells so that the reporter can be expressed. The vector generally transports the nucleic acid to the cells with reduced degradation relative to the extent of degradation that would result in the absence of the vector. In general, the vectors useful in the invention include, but are not limited to, plasmids, phagemids, viruses, other vehicles derived from viral or bacterial sources that have been manipulated by the insertion or incorporation of the antigen nucleic acid sequences. Viral vectors are a preferred type of vector and include, but are not limited

to, nucleic acid sequences from the following viruses: retrovirus, such as Moloney murine leukemia virus, Harvey murine sarcoma virus, murine mammary tumor virus, and Rous sarcoma virus; adenovirus, adeno-associated virus; SV40-type viruses; polyoma viruses; Epstein-Barr viruses; papilloma viruses; herpes virus; vaccinia virus; polio virus; and RNA virus such as a retrovirus. One can readily employ other vectors not named but known in the art.

Preferred viral vectors are based on non-cytopathic eukaryotic viruses in which non-essential genes have been replaced with the gene of interest. Non-cytopathic viruses include retroviruses, the life cycle of which involves reverse transcription of genomic viral RNA into DNA with subsequent proviral integration into host cellular DNA. Retroviruses have been approved for human gene therapy trials. Most useful are those retroviruses that are replication-deficient (i.e., capable of directing synthesis of the desired proteins, but incapable of manufacturing an infectious particle). Such genetically altered retroviral expression vectors have general utility for the high-efficiency transduction of genes *in vivo*. Standard protocols for producing replication-deficient retroviruses (including the steps of incorporation of exogenous genetic material into a plasmid, transfection of a packaging cell lined with plasmid, production of recombinant retroviruses by the packaging cell line, collection of viral particles from tissue culture media, and infection of the target cells with viral particles) are provided in Kriegler, M., Gene Transfer and Expression, A Laboratory Manual W.H. Freeman C.O., New York (1990) and Murray, E.J. Methods in Molecular Biology, vol. 7, Humana Press, Inc., Clifton, New Jersey (1991).

A preferred virus for certain applications is the adeno-associated virus, a double-stranded DNA virus. The adeno-associated virus can be engineered to be replication-deficient and is capable of infecting a wide range of cell types and species. It further has advantages such as, heat and lipid solvent stability; high transduction frequencies in cells of diverse lineages, including hemopoietic cells; and lack of superinfection inhibition thus allowing multiple series of transductions. Reportedly, wild-type adeno-associated virus manifest some preference for integration sites into human cellular DNA, thereby minimizing the possibility of insertional mutagenesis and variability of inserted gene expression characteristic of retroviral infection. In addition, wild-type adeno-associated virus infections have been followed in tissue culture for greater than 100 passages in the absence of selective pressure, implying that the adeno-associated virus genomic integration is a relatively stable event. The adeno-associated virus can also function in an extrachromosomal fashion.

Recombinant adeno-associated viruses that lack the replicase protein apparently lack this integration sequence specificity.

Other vectors include plasmid vectors. Plasmid vectors have been extensively described in the art and are well-known to those of skill in the art. See e.g., Sambrook et al.,
5 Molecular Cloning: A Laboratory Manual, Second Edition, Cold Spring Harbor Laboratory Press, 1989. In the last few years, plasmid vectors have been found to be particularly advantageous for delivering genes to cells *in vivo* because of their inability to replicate within and integrate into a host genome. These plasmids, however, having a promoter compatible with the host cell, can express a peptide from a gene operatively encoded within the plasmid.
10 Some commonly used plasmids include pBR322, pUC18, pUC19, pRc/CMV, SV40, and pBlueScript. Other plasmids are well-known to those of ordinary skill in the art. Additionally, plasmids may be custom designed using restriction enzymes and ligation reactions to remove and add specific fragments of DNA.

In general, the vectors useful in the invention are divided into two classes: biological
15 vectors and chemical/physical vectors. Biological vectors and chemical/physical vectors are useful in the delivery and/or uptake of reporter constructs of the invention.

Most biological vectors are used for delivery of nucleic acids and thus would be most appropriate in the delivery of nucleic acids.

As used herein, a "chemical/physical vector" refers to a natural or synthetic molecule,
20 other than those derived from bacteriological or viral sources, capable of delivering the reference and test compound.

A preferred chemical/physical vector of the invention is a colloidal dispersion system. Colloidal dispersion systems include lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system of the invention is a
25 liposome. Liposomes are artificial membrane vessels which are useful as a delivery vector *in vivo* or *in vitro*. It has been shown that large unilamellar vessels (LUV), which range in size from 0.2 - 4.0 μm can encapsulate large macromolecules. RNA, DNA and intact virions can be encapsulated within the aqueous interior and be delivered to cells in a biologically active form (Fraley, et al., *Trends Biochem. Sci.*, (1981) 6:77).

30 Liposomes may be targeted to a particular tissue by coupling the liposome to a specific ligand such as a monoclonal antibody, sugar, glycolipid, or protein. Ligands which may be useful for targeting a liposome to an immune cell include, but are not limited to, intact or fragments of molecules which interact with immune cell specific receptors and molecules,

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such as antibodies, which interact with the cell surface markers of immune cells. Such ligands may easily be identified by binding assays well known to those of skill in the art. In still other embodiments, the liposome may be targeted to the cancer by coupling it to a one of the immunotherapeutic antibodies discussed earlier. Additionally, the vector may be coupled to a nuclear targeting peptide, which will direct the vector to the nucleus of the host cell.

Lipid formulations for transfection are commercially available from QIAGEN, for example, as EFFECTENE™ (a non-liposomal lipid with a special DNA condensing enhancer) and SUPERFECT™ (a novel acting dendrimeric technology).

Liposomes are commercially available from Gibco BRL, for example, as LIPOFECTIN™ and LIPOFECTACE™, which are formed of cationic lipids such as N-[1-(2, 3 dioleyloxy)-propyl]-N, N, N-trimethylammonium chloride (DOTMA) and dimethyl dioctadecylammonium bromide (DDAB). Methods for making liposomes are well known in the art and have been described in many publications. Liposomes also have been reviewed by Gregoriadis, G. in *Trends in Biotechnology*, (1985) 3:235-241. In some preferred embodiments, the method of choice for delivering DNA (for transfection) to the cells is electroporation, particularly where a stably transfected cell line is sought.

The present invention is further illustrated by the following Examples, which in no way should be construed as further limiting.

Examples

Example 1. Biological Activity of Production Lot of CpG ODN (SEQ ID NO:1) Assayed Using Cells Stably Transfected with hTLR9 Expression Vector

CpG ODN (SEQ ID NO:1) is currently in preclinical and clinical trials for a number of clinical applications. SEQ ID NO:1 has been discovered to induce signaling through TLR9. In order to assess different lots of clinical material, the methods of the invention are employed, using a highly characterized lot of SEQ ID NO:1 as a reference.

In a TLR9 assay, the CpG-non-responsive human embryonal kidney cell line HEK293 (e.g., ATCC CRL-1573) was stably transfected with a hTLR9 expression construct and found to express full-length human TLR9 constitutively. The cells also contained a genomic copy of a reporter construct with a 6x NF-κB binding site and a luciferase gene reporter cassette. Incubation of the cells with CpG ODN (SEQ ID NO:1) activates NF-κB driven expression of luciferase, while incubation with medium alone (negative control) does not. The cells are

then lysed and activity of the luciferase protein determined by its catalytic activity of luciferin oxidation which is measured in a luminometer. Results are expressed as fold induction above medium control.

Assay set-up includes a reference standard material which is highly pure and well characterized. The reference material is used to create a standard curve within a defined range where the dose-response curve is linear (e.g., in the range of the EC₅₀ value for SEQ ID NO:1, 70-100 nM). The test material is dissolved for testing and assayed at a defined concentration. Activity of the test material is calculated using the standard curve of the reference material. Quality of the tested material is deemed acceptable if activity of the test material compared to activity of the reference material falls within predetermined limits.

Example 2. Biological Activity of Production Lot of CpG ODN (SEQ ID NO:1) Assayed Using RPMI 8226 Cells

The assay of Example 1 is performed using RPMI 8226 cells (ATCC CCL-155) in place of the stably transfected HEK cells of Example 1. RPMI 8226 cells naturally express human TLR9. The cells are stably transfected with a 6x NF- κ B-luciferase reporter construct. It is to be understood that the assay could also be carried out by measuring a native readout such as IL-10 secretion.

Example 3. Expression Vectors for Human TLR3 (hTLR3) and Murine TLR3 (mTLR3)

To create an expression vector for human TLR3, human TLR3 cDNA was amplified by the polymerase chain method (PCR) from a cDNA made from human 293 cells using the primers 5'-GAAACTCGAGCCACCATGAGACAGACTTTGCCTTGTATCTAC-3' (sense, SEQ ID NO:152) and 5'-GAAAGAATTCTTAATGTACAGAGTTTTTGGATCCAAG-3' (antisense, SEQ ID NO:153). The primers introduce *Xho*I and *Eco*RI restriction endonuclease sites at their 5' ends for use in subsequent cloning into the expression vector. The resulting amplification product fragment was cloned into pGEM-T Easy vector (Promega), isolated, cut with *Xho*I and *Eco*RI restriction endonucleases, ligated into an *Xho*I/*Eco*RI-digested pcDNA3.1 expression vector (Invitrogen). The insert was fully sequenced and translated into protein. The cDNA sequence corresponds to the published cDNA sequence for hTLR3, available as GenBank accession no. NM_003265 (SEQ ID NO:7). The open reading frame codes for a protein 904 amino acids long, having the sequence corresponding to GenBank accession no. NP_003256 (SEQ ID NO:8).

Corresponding nucleotide and amino acid sequences for murine TLR3 (mTLR3) are known. The nucleotide sequence of mTLR3 cDNA has been reported as GenBank accession no. AF355152 (SEQ ID NO:9), and the amino acid sequence of mTLR3 has been reported as GenBank accession no. AAK26117 (SEQ ID NO:10).

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Example 4. Reconstitution of TLR3 Signaling in 293 Fibroblasts

Human TLR3 cDNA and murine TLR3 cDNA in pT-Adv vector (from Clontech) were individually cloned into the expression vector pcDNA3.1(-) from Invitrogen using the *EcoRI* site. The resulting expression vectors mentioned above were transfected into
10 CpG-DNA non-responsive human 293 fibroblast cells (ATCC, CRL-1573) using the calcium phosphate method. Utilizing a “gain of function” assay it was possible to reconstitute human TLR3 (hTLR3) and murine TLR3 (mTLR3) signaling in 293 fibroblast cells.

Since NF- κ B activation is central to the IL-1/TLR signal transduction pathway (Medzhitov R et al. (1998) *Mol Cell* 2:253-8; Muzio M et al. (1998) *J Exp Med*
15 187:2097-101), in a first set of experiments human 293 fibroblast cells were transfected with hTLR3 alone or co-transfected with hTLR3 and an NF- κ B-driven luciferase reporter construct.

Likewise, in a second set of experiments, 293 fibroblast cells were transfected with hTLR3 alone or co-transfected with hTLR3 and an IFN- α 4-driven luciferase reporter
20 construct (described in Example 8 below).

In a third group of experiments, 293 fibroblast cells were transfected with hTLR3 alone or co-transfected with hTLR3 and a RANTES-driven luciferase reporter construct (described in Example 14 below).

25 Example 5. Reconstitution of TLR7 Signaling

Methods for cloning murine and human TLR7 have been described in pending U.S. Pat. Application No. 09/954,987 and corresponding published PCT application PCT/US01/29229 (WO 02/22809), both filed September 17, 2001, the contents of which are incorporated herein by reference. Human TLR7 cDNA and murine TLR7 cDNA in pT-Adv
30 vector (from Clontech) were individually cloned into the expression vector pcDNA3.1(-) from Invitrogen using the *EcoRI* site. Utilizing a “gain of function” assay it was possible to reconstitute human TLR7 (hTLR7) and murine TLR7 (mTLR7) signaling in CpG-DNA non-responsive human 293 fibroblasts (ATCC, CRL-1573). The expression vectors

mentioned above were transfected into 293 fibroblast cells using the calcium phosphate method.

Example 6. Reconstitution of TLR8 Signaling

5 Methods for cloning murine and human TLR8 have been described in pending U.S. Pat. Application No. 09/954,987 and corresponding published PCT application PCT/US01/29229 (WO 02/22809), both filed September 17, 2001, the contents of which are incorporated by reference. Human TLR8 cDNA and murine TLR8 cDNA in pT-Adv vector (from Clontech) were individually cloned into the expression vector pcDNA3.1(-) from
10 Invitrogen using the EcoRI site. Utilizing a “gain of function” assay it was possible to reconstitute human TLR8 (hTLR8) and murine TLR8 (mTLR8) signaling in CpG-DNA non-responsive human 293 fibroblasts (ATCC, CRL-1573). The expression vectors mentioned above were transfected into 293 fibroblast cells using the calcium phosphate method.

Example 7. Reconstitution of TLR9 Signaling in 293 Fibroblasts

 Methods for cloning murine and human TLR9 have been described in pending U.S. Pat. Application No. 09/954,987 and corresponding published PCT application PCT/US01/29229 (WO 02/22809), both filed September 17, 2001, the contents of which are
20 incorporated by reference. Human TLR9 cDNA and murine TLR9 cDNA in pT-Adv vector (from Clontech) were individually cloned into the expression vector pcDNA3.1(-) from Invitrogen using the EcoRI site. Utilizing a “gain of function” assay it was possible to reconstitute human TLR9 (hTLR9) and murine TLR9 (mTLR9) signaling in CpG-DNA non-responsive human 293 fibroblasts (ATCC, CRL-1573). The expression vectors
25 mentioned above were transfected into 293 fibroblast cells using the calcium phosphate method.

 To generate stable clones expressing human TLR9, murine TLR9, or either TLR9 with the NF- κ B-luc reporter plasmid, 293 cells were transfected in 10 cm plates (2×10^6 cells/plate) with 16 μ g of DNA and selected with 0.7 mg/ml G418 (PAA Laboratories GmbH, Cölbe,
30 Germany). Clones were tested for TLR9 expression by RT-PCR, for example as shown in Fig. 21. The clones were also screened for IL-8 production or NF- κ B-luciferase activity after stimulation with ODN. Four different types of clones were generated.

293-hTLR9-luc: expressing human TLR9 and 6x NF- κ B-luciferase reporter
 293-mTLR9-luc: expressing murine TLR9 and 6x NF- κ B-luciferase reporter
 293-hTLR9: expressing human TLR9
 293-mTLR9: expressing murine TLR9

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Human 293 fibroblast cells were transiently transfected with hTLR9 and a 6x NF- κ B-luciferase reporter plasmid (NF- κ B-luc, kindly provided by Patrick Baeuerle, Munich, Germany) (Fig. 18A) or with hTLR9 alone (Fig. 18B). After stimulus with CpG-ODN (2 μ M, TCGTCGTTTTGTCGTTTTGTCGTT, SEQ ID NO:1), GpC-ODN (2 μ M, TGCTGCTTTTGTGCTTTTGTGCTT, SEQ ID NO:154), LPS (100 ng/ml) or media, NF- κ B activation by luciferase readout (8h, Fig. 18A) or IL-8 production by ELISA (48h, Fig. 18B) was monitored. Results are representative of three independent experiments. Fig. 18 shows that cells expressing hTLR9 responded to CpG-DNA but not to LPS.

10

Human 293 fibroblast cells were transiently transfected with mTLR9 and the NF- κ B-luc construct. Similar data was obtained for IL-8 production (not shown). Thus expression of TLR9 (human or mouse) in 293 cells results in a gain of function for CpG DNA stimulation similar to hTLR4 reconstitution of LPS responses.

15

Figs. 19 and 20 demonstrate the responsiveness of a stable 293-mTLR9-luc and 293-hTLR9-luc clones after stimulation with CpG-ODN (2 μ M, SEQ ID NO:1), GpC-ODN (2 μ M, SEQ ID NO:154), Me-CpG-ODN (2 μ M; TZGTZGTTTTGTZGTTTTGTZGTT, Z = 5-methylcytidine, SEQ ID NO:147), LPS (100 ng/ml) or media, as measured by monitoring NF- κ B activation. Similar results were obtained utilizing IL-8 production with the stable clones. These results demonstrate that CpG-DNA non-responsive cell lines can be stably genetically complemented with TLR9 to become responsive to CpG DNA in a motif-specific manner.

20

25

Example 8. Method of Making IFN- α Reporter Vector

A number of reporter vectors may be used in the practice of the invention. Some of the reporter vectors are commercially available, e.g., the luciferase reporter vectors pNF- κ B-Luc (Stratagene) and pAP1-Luc (Stratagene). These two reporter vectors place the luciferase gene under control of an upstream (5') promoter region derived from genomic DNA for NF- κ B or AP1, respectively. Other reporter vectors can be constructed following standard

30

methods using the desired promoter and a vector containing a suitable reporter, such as luciferase, β -galactosidase (β -gal), chloramphenicol acetyltransferase (CAT), and other reporters known by those skilled in the art. Following are some examples of reporter vectors constructed for use in the present invention.

5 IFN- α 4 is an immediate-early type 1 IFN. Sequence-specific PCR products for the –620 to +50 promoter region of IFN- α 4 were derived from genomic DNA of human 293 cells and cloned into the *Sma*I site of the pGL3-Basic Vector (Promega). The resulting expression vector includes a luciferase gene under control of an upstream (5') –620 to +50 promoter region of IFN- α 4. The sequence of the –620 to +50 promoter region of IFN- α 4 is provided as
10 SEQ ID NO:121.

Example 9. Method of Making IFN- α 1 Reporter Vector

IFN- α 1 is a late type 1 IFN. Sequence-specific PCR products for the –140 to +9 promoter region of IFN- α 1 were derived from genomic DNA of human 293 cells and cloned
15 into *Sma*I site of the pGL3-Basic Vector (Promega). The resulting expression vector includes a luciferase gene under control of an upstream (5') –140 to +9 promoter region of IFN- α 1. A sequence of the –140 to +9 promoter region of IFN- α 1 is provided as SEQ ID NO:122.

Example 10. Method of Making IFN- β Reporter Vector

20 IFN- β is an immediate-early type 1 IFN. The –280 to +20 promoter region of IFN- β was derived from the pUC β 26 vector (Algaré M et al. (1999) *J Virol* 73:2694-702) by restriction at *Eco*RI and *Taq*I sites. The 300 bp restriction fragment was filled in by Klenow enzyme and cloned into *Nhe*I-digested and filled in pGL3-Basic Vector (Promega). The resulting expression vector includes a luciferase gene under control of an upstream (5') –280
25 to +20 promoter region of IFN- β . A sequence of the –280 to +20 promoter region of IFN- β is provided as SEQ ID NO:123.

Example 11. Method of Making Human IL-6 Reporter Vectors

Reporter constructs are made using the –285 to +7 promoter region derived from
30 human IL-6 genomic DNA. (Takeshita et al. Eur. J. Immunol. 2000. 30: 108–116.) In one reporter construct the IL-6 promoter region is cloned as a *Kpn*I-*Xho*I insert into pGL3-Basic Vector (Promega). The resulting expression vector includes a luciferase gene under control of

an upstream (5') -288 to +7 promoter region derived from human IL-6 genomic DNA. A sequence of the -288 to +7 promoter region of human IL-6 is provided as SEQ ID NO:128.

The promoter can also be derived from the full-length promoter region of the IL-6 gene from -1174 to +7 (GenBank Accession No M22111) as shown below as SEQ ID NO:129.

Example 12. Method of Making Human IL-8 Reporter Vectors

Reporter constructs have been made using a -546 to +44 and a truncated -133 to +44 promoter region derived from human IL-8 genomic DNA. Mukaida N et al. (1989) *J Immunol* 143:1366-71. In each reporter construct the IL-8 promoter region was cloned as a *KpnI-XhoI* insert into pGL3-Basic Vector (Promega). One of the resulting expression vectors includes a luciferase gene under control of an upstream (5') -546 to +44 promoter region derived from human IL-8 genomic DNA. Another of the resulting expression vectors includes a luciferase gene under control of an upstream (5') -133 to +44 promoter region derived from human IL-8 genomic DNA.

The promoter can also be the upstream (5') -734 to +44 or the upstream (5') -162 to +44 promoter region derived from human IL-8 genomic DNA. Mukaida N et al. (1989) *J Immunol* 143:1366-71. A sequence of the -734 to +44 promoter region derived from human IL-8 is provided below as SEQ ID NO: 130.

Example 13. Method of Making Human IL-12 p40 Reporter Vectors

Reporter constructs have been made using truncated (-250 to +30, SEQ ID NO:127) and full length (-751 to +30, SEQ ID NO:126) promoter regions derived from human IL-12 p40 genomic DNA. (Takeshita et al. *Eur. J. Immunol.* 2000. 30: 108-116.) In one reporter construct the truncated IL-12 p40 promoter was cloned as a *KpnI-XhoI* insert into p β gal-Basic (Promega). The resulting expression vector includes a β gal gene under control of an upstream (5') -250 to +30 promoter region of human IL-12 p40. In a second reporter construct the full length IL-12 p40 promoter was cloned as a *KpnI-XhoI* insert into p β gal-Basic (Promega). The resulting expression vector includes a β gal gene under control of an upstream (5') -751 to +30 promoter region of human IL-12 p40. In a third reporter construct the truncated -250 to +30 promoter region of human IL-12 p40 was cloned into the pGL3-Basic Vector (Promega). The resulting expression vector includes a luciferase gene under control of an upstream (5') -250 to +30 promoter region of human IL-12 p40. In a

fourth reporter construct the full length IL-12 p40 promoter of human IL-12 p40 was cloned into the pGL3-Basic Vector (Promega). The resulting expression vector includes a luciferase gene under control of an upstream (5') -751 to +30 promoter region of human IL-12 p40. A sequence of the -751 to +30 promoter region of human IL-12 p40 is provided as SEQ ID NO: 126.

Example 14. Method of Making RANTES Reporter Vector

Transcription of the chemokine RANTES is believed to be regulated at least in part by IRF3 and by NF- κ B. Lin R et al. (1999) *J Mol Cell Biol* 19(2):959-66; Genin P et al. (2000) *J Immunol* 164:5352-61. A 483 bp sequence-specific PCR product including the -397 to +5 promoter region of RANTES was derived from genomic DNA of human 293 cells, restricted with *Pst*I and cloned into pCAT-Basic Vector (Promega) using *Hind*III (filled in with Klenow) and *Pst*I sites (filled in). The -397 to +5 promoter region of RANTES was then isolated from the resulting RANTES/chloramphenicol acetyltransferase (CAT) reporter plasmid by restriction with *Bgl*II and *Sal*I, filled in with Klenow enzyme, and cloned into the *Nhe*I site (filled in with Klenow) of the pGL3-Basic Vector (Promega). The resulting expression vector includes a luciferase gene under control of an upstream (5') -397 to +5 promoter region of RANTES. Comparison of the insert sequence -397 to +5 of Genin P et al. (2000) *J Immunol* 164:5352-61 and GenBank accession no. AB023652 (SEQ ID NO:125) revealed two point deletions (at positions 105 and 273 of SEQ ID NO:125) which do not create new restriction sites. A sequence of the -397 to +5 promoter region of RANTES is provided as SEQ ID NO:125.

Example 15. RT-PCR Analysis of Cell Lines for TLR Expression

TLR expression was determined using total RNA of cells prepared by standard methods (QIAGEN). RNA was transcribed to cDNA using AMV Reverse Transcriptase (Roche). Quantitative PCR was performed with TLR-gene specific primer sets using a LightCycler Instrument (Roche). Controls for genomic DNA impurities were performed by a similar PCR method using RNA (but without reverse transcriptase).

A variety of cell lines was screened for their expression of TLR3, 7, 8 and 9. These cell lines are A549 (human lung carcinoma), BeWo (human choriocarcinoma), HeLa (human cervix carcinoma), Hep-2 (human cervix carcinoma), KG-1 (human acute myeloid leukemia), MUTZ-3 (human acute myelomonocytic leukemia), Nalm-6 (human B cell precursor

leukemia), NK-92 (human Natural killer cell line), NK-92 MI (human Natural killer cell line, IL-2 independent), Raji (human Burkitt's lymphoma, B lymphocyte), RAMOS (Burkitt's lymphoma, B lymphocyte), RPMI 8226 (human multiple myeloma, B lymphocyte), THP-1 (human acute monocytic leukemia), U937 (human lymphoma) and Jurkat (human T cell leukemia).

All B cell lines express, as determined by Real Time-PCR (RT-PCR), endogenous TLR9. In addition, all lines except NALM co-express TLR7. Nevertheless, none of the other cell lines appeared to express TLR7, whereas low TLR9 expression on the mRNA level was observed for KG-1 and THP-1. TLR3 appeared to be expressed in most of these cell lines, with the highest mRNA levels for example in the NK cell lines (e.g., NK-92).

Raji cells contain high levels of TLR9 mRNA and low levels of TLR3 and TLR7 mRNA suggesting high expression of TLR9 protein and lower levels of TLR3 and TLR7 protein.

These results indicate that the cell lines expressing TLR9 can be used to screen potential new TLR9 ligands (CpG ODN, etc.), cell lines expressing TLR7 to screen potential new TLR7 ligands (ORN (oligoribonucleotides), small molecules, etc.), and cell lines expressing both receptors may be used to screen for "hybrid" TLR7 and 9 agonists. In addition, cell lines lacking TLR8 expression (i.e., all cell lines tested) can be used to confirm the specificity of a TLR7 versus a TLR8 ligand (i.e., the latter should not be able to stimulate TLR7-expressing cells). In contrast, cell lines expressing TLR3 (e.g., Raji cells) may be used to screen for potential new TLR3 ligands (dsRNA, etc.).

Example 16. Screening of Various Cell Lines for Responses to TLR Ligands

Except where otherwise indicated, the following general methods were used.

Cells were plated at 5×10^5 /ml in 48 well plates in RPMI medium with 10% FBS. Stimulation was performed by addition of the oligonucleotides or other compounds diluted to the test concentrations in TE. Cells were incubated for 24 or 48h and the supernatants were taken to analyse for the presence of cytokines or chemokines.

The TLR ligands used are as follows:

TLR3: Poly I:C

TLR7, TLR8: R-848

TLR9:

T*C*C*A*G*G*A*C*T*T*C*T*C*T*C*A*G*G*T*T (SEQ ID NO: 2);

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T*C*G*T*C*G*T*T*T*T*G*T*C*G*T*T*T*T*G*T*C*G*T*T (SEQ ID NO: 1);
 T*G*C*T*G*C*T*T*T*T*G*T*G*C*T*T*T*T*G*T*G*C*T*T (SEQ ID NO: 154);
 T*C*G*T*C*G*T*T*T*T*C*G*G*C*G*C*G*C*G*C*C*G (SEQ ID NO: 158);
 G*G*G_G_A_C_G_A_C_G_T_C_G_T_G_G*G*G*G*G*G (SEQ ID NO: 159);
 5 T*G*C*T*G*C*T*T*T*T*C*G*G*C*G*G*C*C*G*C*C*G (SEQ ID NO: 160);
 G*G*G_G_A_G_C_A_G_C_T_G_C_T_G_G*G*G*G*G*G (SEQ ID NO: 161).
 * phosphorothioate linkage; _ phosphodiester linkage.

Increased expression of cell surface markers was determined using cells stimulated as
 10 described above and then stained with different monoclonal antibody combinations specific
 for the cell surface markers. Analysis of the cells was performed by flow cytometry.

Changes in reporter gene activity were determined using cells transfected with a
 NF- κ B reporter construct (Stratagene) and a β -galactosidase reporter control plasmid
 (Invitrogen) using electroporation. For NF- κ B analysis, a 5x NF- κ B-Luciferase Vector
 15 (Stratagene) was used. The amount of DNA transfected as well as cell concentration was
 varied. Stimulation was performed 24h after transfection. Cells were stimulated with the
 indicated amounts of ODN, R-848, LPS, TNF- α , or IL-1 β for the indicated incubation times.
 Cell extracts were prepared by lysing the cells in 100 μ l reporter lysis buffer (Promega) using
 the freeze-thaw method. All data were normalized for β -galactosidase expression.
 20 Stimulation indices were calculated in reference to luciferase activity of medium without
 addition of ODN.

Stimulation of the Raji cell line with a TLR9 ligand (CpG ODN), a TLR3 ligand (poly
 I:C) or a TLR7 ligand (R-848) results in the ligand-specific secretion of cytokines. Figs. 14
 and 15 show IL-6 production of Raji cells upon stimulation with ODN, poly I:C or R-848.
 25 Fig. 16 shows IFN- α 2 production of Raji cells upon stimulation with ODN, poly I:C or R-848.
 In all assays, cells were incubated with Na-Butyrate for 48h before stimulation with TLR
 ligands. CpG stimulation of the RAMOS cell lines can result in the CpG-specific up-
 regulation of cell surface markers such as CD80, as shown in Fig. 17.

30 **Example 17. Inhibition of a Positive Reference Compound Response with an Inhibitory Test Compound**

Inhibition of CpG mediated chemokine production was determined using RPMI 8226
 cells incubated with increasing amounts of SEQ ID NO:1 in the presence of an

immunoinhibitory ODN (SEQ ID NO: 151). IP-10 production was measured 24h later by ELISA (Fig. 9).

Equivalents

5 The foregoing written specification is considered to be sufficient to enable one skilled in the art to practice the invention. The present invention is not to be limited in scope by examples provided, since the examples are intended as a single illustration of one aspect of the invention and other functionally equivalent embodiments are within the scope of the invention. Various modifications of the invention in addition to those shown and described
10 herein will become apparent to those skilled in the art from the foregoing description and fall within the scope of the appended claims. The advantages and objects of the invention are not necessarily encompassed by each embodiment of the invention.

 All references, patents and patent publications that are recited in this application are incorporated in their entirety herein by reference.

15

 We claim:

Claims

1. A screening method for identifying agonists of Toll-like receptor (TLR) signaling activity, comprising

contacting an RPMI 8226 cell that expresses a TLR with a test compound and
5 measuring a test level of TLR signaling activity,
wherein a test level that is positive is indicative of a test compound that is a TLR agonist, and

wherein the TLR signaling activity is selected from the group consisting of CD71 expression, CD86 expression, HLA-DR expression, IL-8 expression, IL-8 production, IL-8
10 secretion, IL-10 expression, IL-10 production, IL-10 secretion, IP-10 expression, IP-10 production, IP-10 secretion, TNF- α expression, TNF- α production and TNF- α secretion.

2. A screening method for identifying agonists of Toll-like receptor (TLR) signaling activity, comprising

15 contacting a cell that expresses a TLR with a test compound and measuring a test level of TLR signaling activity,
wherein a test level that is positive is indicative of an immunostimulatory compound, and

wherein the cell is a Raji cell, a RAMOS cell, a Nalm cell, a THP-1 cell, or a KG-
20 1 cell.

3. The method of claim 1 or 2, wherein the test level is positive relative to a reference level determined by contacting the cell with a reference compound and measuring a reference TLR signaling activity.

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4. The method of claim 3, wherein the reference compound is a positive reference compound

5. The method of claim 4, wherein the positive reference compound is
30 selected from the group consisting of an immunostimulatory nucleic acid and an imidazoquinoline compound.

6. The method of claim 3, wherein the reference compound is a negative reference compound.

7. The method of claim 6, wherein the negative reference compound is medium alone.

8. The method of claim 5, wherein the immunostimulatory nucleic acid is selected from the group consisting of a CpG nucleic acid, a T-rich nucleic acid, a poly-T nucleic acid and a poly-G nucleic acid.

9. The method of claim 5, wherein the imidazoquinoline compound is selected from the group consisting of R-848 and R-847.

10. The method of claim 1 or 2, wherein the test compound is a nucleic acid.

11. The method of claim 10, wherein the nucleic acid does not comprise a motif selected from the group consisting of a CpG motif, a poly-T motif, a T-rich motif and a poly-G motif.

12. The method of claim 10, wherein the nucleic acid comprises a phosphorothioate backbone linkage.

13. The method of claim 10, wherein the nucleic acid is a DNA, an RNA or a DNA-RNA hybrid.

14. The method of claim 1 or 2, wherein the test compound is a non-nucleic acid small molecule.

15. The method of claim 1 or 2, wherein the test compound comprises an amino acid, a carbohydrate, a lipid, or a hormone.

16. The method of claim 15, wherein the carbohydrate is a polysaccharide.

17. The method of claim 1 or 2, wherein the test compound is derived from a molecular library.

5 18. The method of claim 1, wherein the cell is transfected with a nucleic acid.

19. The method of claim 18, wherein the nucleic acid encodes a TLR or a reporter construct.

10 20. The method of claim 2, wherein the cell is transfected with a nucleic acid.

15 21. The method of claim 20, wherein the nucleic acid encodes a TLR or a reporter construct.

22. The method of claim 19 or 21, wherein the TLR is selected from the group consisting of TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9 and TLR10.

20 23. The method of claim 22, wherein the TLR is a human TLR.

24. The method of claim 19 or 21, wherein the reporter construct is selected from the group consisting of a luciferase reporter construct, a β -galactosidase reporter construct, a chloramphenicol acetyltransferase reporter construct, a green fluorescent protein reporter construct, and a secreted alkaline phosphatase construct.

25 25. The method of claim 19 or 21, wherein the reporter construct comprises a TLR responsive promoter.

30 26. The method of claim 25, wherein the TLR responsive promoter comprises a transcription factor binding site selected from the group consisting of a NF- κ B binding site, an AP-1 binding site, a CRE, a SRE, an ISRE, a GAS, an ATF2 binding site, an

IRF3 binding site, an IRF7 binding site, an NFAT binding site, a p53 binding site, an SRF binding site, and a TARE.

27. The method of claim 25, wherein the TLR responsive promoter is a
5 promoter region selected from the group consisting of an IL-1 promoter region, an IL-6 promoter region, an IL-8 promoter region, an IL-10 promoter region, an IL-12 p40 promoter region, an IFN- α 1 promoter region, an IFN- α 4 promoter region, an IFN- β promoter region, an IFN- γ promoter region, a TNF- α promoter region, a TNF- β promoter region, an IP-9 promoter region, an IP-10 promoter region, a RANTES promoter region, an ITAC promoter region, a
10 MCP-1 promoter region, an IGFBP4 promoter region, a CD54 promoter region, a CD69 promoter region, a CD71 promoter region, a CD80 promoter region, a CD86 promoter region, a HLA-DR promoter region, and a HLA class I promoter region.

28. The method of claim 18 or 20, wherein the cell is stably transfected.
15

29. The method of claim 1 or 2, wherein the TLR signaling activity is measured by cytokine secretion or chemokine secretion.

30. The method of claim 1, wherein the TLR signaling activity is selected
20 from the group consisting of IL-8 secretion, IL-10 secretion, IP-10 secretion and TNF- α secretion.

31. The method of claim 2, wherein the TLR signaling activity is selected
from the group consisting of IL-6 expression, IL-6 production, IL-6 secretion, IL-8
25 expression, IL-8 production, IL-8 secretion, IL-10 expression, IL-10 production, IL-10 secretion, IP-10 expression, IP-10 production, IP-10 secretion, IL-12 expression, IL-12 production, IL-12 secretion, TNF- α expression, TNF- α production and TNF- α secretion.

32. The method of claim 2, wherein the TLR signaling activity is measured
30 by phosphorylation.

33. The method of claim 32, wherein phosphorylation is total cellular phosphorylation.

34. The method of claim 32, wherein phosphorylation is phosphorylation of a factor selected from the group consisting of IRAK, ERK, MyD88, TRAF6, p38, NFkB subunits, c-Jun and c-Fos.

5

35. The method of claim 1 or 2, wherein the TLR signaling activity is measured by gene expression.

36. The method of claim 1, wherein the TLR signaling activity is measured
10 by gene expression selected from the group consisting of CD71 expression, CD86 expression, HLA-DR expression, IL-8 expression, IL-10 expression, IP-10 expression, and TNF- α expression.

37. The method of claim 35, wherein TLR signaling activity is measured
15 by microarray techniques.

38. The method of claim 2, wherein the TLR signaling activity is measured by cell proliferation.

20 39. The method of claim 1 or 2, wherein TLR signaling activity is measured by cell surface marker expression.

40. The method of claim 1, wherein TLR signaling activity is measured by cell surface expression of CD71, CD86 or HLA-DR.

25

41. The method of claim 2, wherein TLR signaling activity is measured by CD71 cell surface expression, CD86 cell surface expression, HLA-DR cell surface expression, CD80 cell surface expression, HLA class I cell surface expression, CD54 cell surface expression and CD69 cell surface expression.

30

42. The method of claim 2, wherein TLR signaling activity is measured by antibody secretion.

43. The method of claim 42, wherein the antibody secretion is IgM secretion.

44. A composition comprising
an RPMI 8226 cell stably transfected with a nucleic acid encoding a TLR

5 polypeptide, or a fragment thereof.

45. The composition of claim 44, further comprising a reporter construct
comprising a promoter and a reporter sequence wherein the promoter is a TLR responsive
promoter.

10

46. The composition of claim 45, wherein the TLR responsive promoter
comprises a nucleic acid sequence selected from the group consisting of an NF- κ B binding
site, an AP-1 binding site, a CRE, a SRE, an ISRE, a GAS, an ATF2 binding site, an IRF3
binding site, an IRF7 binding site, an NFAT binding site, a p53 binding site, an SRF binding
15 site, and a TARE.

47. The composition of claim 45, wherein the reporter sequence is selected
from the group consisting of a luciferase sequence, a β -galactosidase sequence, a green
fluorescent protein sequence, a secreted alkaline phosphatase sequence and a chloramphenicol
20 transferase sequence.

48. The composition of claim 44, wherein the TLR polypeptide or fragment
thereof is a human TLR polypeptide or fragment thereof.

25 49. The composition of claim 44, wherein the TLR polypeptide or fragment
thereof is selected from the group consisting of TLR1, TLR2, TLR3, TLR4, TLR5, TLR6,
TLR7, TLR8, TLR9 and TLR10.

30 50. The composition of claim 44, wherein the TLR polypeptide or fragment
thereof is a human TLR polypeptide.

51. A screening method for identifying agonists of Toll-like receptor (TLR)
signaling activity, comprising

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contacting an cell that ectopically expresses a TLR with a test compound and measuring a test level of TLR signaling activity,

wherein a test level that is positive is indicative of a test compound that is a TLR agonist, and

5 wherein the cell that ectopically expresses a TLR is selected from the group consisting of RPMI 8226, RAMOS, Raji, Nalm, THP-1, KG-1 and 293 HEK.

52. The method of claim 51, wherein the test level is positive relative to a reference level determined by contacting the cell with a reference compound and measuring a
10 reference TLR signaling activity.

53. The method of claim 52, wherein the reference compound is a positive reference compound.

15 54. The method of claim 53, wherein the positive reference compound is selected from the group consisting of an immunostimulatory nucleic acid and an imidazoquinoline compound.

20 55. The method of claim 54, wherein the immunostimulatory nucleic acid is selected from the group consisting of a CpG nucleic acid, a T-rich nucleic acid, a poly-T nucleic acid and a poly-G nucleic acid.

25 56. The method of claim 54, wherein the imidazoquinoline compound is selected from the group consisting of R-848 and R-847.

57. The method of claim 52, wherein the reference compound is negative reference compound.

30 58. The method of claim 57, wherein the negative reference compound is medium alone.

59. The method of claim 51, wherein the test compound is a nucleic acid.

60. The method of claim 59, wherein the nucleic acid does not comprise a motif selected from the group consisting of a CpG motif, a poly-T motif, a T-rich motif and a poly-G motif.

5 61. The method of claim 59, wherein the nucleic acid comprises a phosphorothioate backbone linkage.

62. The method of claim 59, wherein the nucleic acid is a DNA, an RNA, or a DNA-RNA hybrid.

10 63. The method of claim 51, wherein the test compound is a non-nucleic acid small molecule.

64. The method of claim 51, wherein the test compound comprises an
15 amino acid, a carbohydrate, a lipid, or a hormone.

65. The method of claim 64, wherein the carbohydrate is a polysaccharide.

66. The method of claim 51, wherein the test compound is derived from a
20 molecular library.

67. The method of claim 51, wherein the TLR signaling activity is selected from the group consisting of CD71 expression, CD86 expression, HLA-DR expression, IL-6 expression, IL-6 production, IL-6 secretion, IL-8 expression, IL-8 production, IL-8 secretion,
25 IL-10 expression, IL-10 production, IL-10 secretion, IL-12 expression, IL-12 production, IL-12 secretion, IP-10 expression, IP-10 production, IP-10 secretion, TNF- α expression, TNF- α production and TNF- α secretion.

68. The method of claim 51, wherein the TLR is selected from the group
30 consisting of TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9 and TLR10.

69. The method of claim 51, wherein the TLR is a human TLR.

70. The method of claim 51, wherein the cell is transfected with a reporter construct.

71. The method of claim 70, wherein the reporter construct is selected from the group consisting of a luciferase reporter construct, a β -galactosidase reporter construct, a chloramphenicol acetyltransferase reporter construct, a green fluorescent protein reporter construct, and a secreted alkaline phosphatase construct.

72. The method of claim 71, wherein the TLR signaling activity is measured by luciferase expression, β -galactosidase expression, chloramphenicol expression, acetyltransferase expression, green fluorescent protein expression, alkaline phosphatase expression and alkaline phosphatase secretion.

73. The method of claim 71, wherein the reporter construct comprises a TLR responsive promoter.

74. The method of claim 25 or 73, wherein the TLR responsive promoter is a TLR1 responsive promoter, a TLR2 responsive promoter, a TLR3 responsive promoter, a TLR4 responsive promoter, a TLR5 responsive promoter, a TLR6 responsive promoter, a TLR7 responsive promoter, a TLR8 responsive promoter, a TLR9 responsive promoter and a TLR10 responsive promoter.

75. The method of claim 73, wherein the TLR responsive promoter comprises a transcription factor binding site selected from the group consisting of an NF- κ B binding site, an AP-1 binding site, a CRE, a SRE, an ISRE, a GAS, an ATF2 binding site, an IRF3 binding site, an IRF7 binding site, an NFAT binding site, a p53 binding site, an SRF binding site, and a TARE.

76. The method of claim 73, wherein the TLR responsive promoter is a promoter region selected from the group consisting of an IL-1 promoter region, an IL-6 promoter region, an IL-8 promoter region, an IL-10 promoter region, an IL-12 p40 promoter region, an IFN- α 1 promoter region, an IFN- α 4 promoter region, an IFN- β promoter region, an IFN- γ promoter region, a TNF- α promoter region, a TNF- β promoter region, an IP-9 promoter

region, an IP-10 promoter region, a RANTES promoter region, an ITAC promoter region, a MCP-1 promoter region, an IGFBP4 promoter region, a CD54 promoter region, a CD69 promoter region, a CD71 promoter region, a CD80 promoter region, a CD86 promoter region, a HLA-DR promoter region, and a HLA class I promoter region.

5

77. The method of claim 51, wherein the cell is stably transfected with a TLR nucleic acid.

10

78. The method of claim 70, wherein the cell is stably transfected with the reporter construct.

79. The method of claim 51, wherein the TLR signaling activity is measured by cytokine secretion or chemokine secretion.

15

80. The method of claim 79, wherein the cytokine secretion or chemokine secretion is selected from the group consisting of IL-8 secretion, TNF- α secretion, IL-10 secretion and IP-10 secretion.

20

81. The method of claim 79, wherein the cytokine secretion or chemokine secretion is selected from the group consisting of IL-6 secretion and IL-12 secretion.

82. The method of claim 51, wherein the TLR signaling activity is measured by phosphorylation.

25

83. The method of claim 82, wherein phosphorylation is total cellular phosphorylation.

30

84. The method of claim 82, wherein phosphorylation is phosphorylation of a factor selected from the group consisting of IRAK, ERK, MyD88, TRAF6, p38, NF- κ B subunits, c-Jun and c-Fos.

85. The method of claim 51, wherein the TLR signaling activity is measured by gene expression.

86. The method of claim 85, wherein the gene expression is selected from the group consisting of IL-8 expression, IL-10 expression, IP-10 expression, CD71 expression, CD86 expression and HLA-DR expression.

5

87. The method of claim 85, wherein the gene expression is selected from the group consisting of IL-6 expression, IL-12 expression and TNF- α expression.

88. The method of claim 51, wherein the TLR signaling activity is
10 measured by microarray techniques.

89. The method of claim 51, wherein the TLR signaling activity is measured by cell proliferation.

90. The method of claim 51, wherein the TLR signaling activity is
15 measured by cell surface marker expression.

91. The method of claim 90, wherein the cell surface marker expression is selected from the group consisting of CD71 cell surface expression, CD86 cell surface
20 expression and HLA-DR cell surface expression.

92. The method of claim 90, wherein the cell surface marker expression is selected from the group consisting of CD80 cell surface expression, HLA class I cell surface expression, CD54 cell surface expression and CD69 cell surface expression.
25

93. The method of claim 51, wherein the TLR signaling activity is measured by antibody secretion.

94. The method of claim 93, wherein the antibody secretion is IgM
30 secretion.

95. A screening method for identifying antagonists of Toll-like receptor (TLR) signaling activity, comprising

contacting a cell with a positive reference compound and measuring a reference level of TLR signaling activity,

contacting the cell with the positive reference compound and a test compound, and measuring a test level of TLR signaling activity,

5 wherein a test level that is less than a reference level is indicative of test compound that is a TLR antagonist, and

wherein the cell is selected from the group consisting of a RPMI 8226 cell, a RAMOS cell, a Raji cell, a THP-1 cell, a Nalm cell and a KG-1 cell.

10 96. The method of claim 95, wherein the positive reference compound is selected from the group consisting of an immunostimulatory nucleic acid and an immunostimulatory imidazoquinoline compound.

15 97. The method of claim 96, wherein the immunostimulatory nucleic acid is selected from the group consisting of a CpG nucleic acid, a T-rich nucleic acid, a poly-T nucleic acid and a poly-G nucleic acid.

98. The method of claim 96, wherein the imidazoquinoline compound is selected from the group consisting of R-848 and R-847.

20 99. The method of claim 95, wherein the test compound is a nucleic acid.

100. The method of claim 99, wherein the nucleic acid does not comprise a motif selected from the group consisting of a CpG motif, a poly-T motif, a T-rich motif and a poly-G motif.

101. The method of claim 99, wherein the nucleic acid comprises a phosphorothioate backbone linkage.

30 102. The method of claim 99, wherein the nucleic acid is a DNA, an RNA or a DNA-RNA hybrid.

103. The method of claim 95, wherein the test compound is a non-nucleic acid small molecule.

104. The method of claim 95, wherein the test compound comprises an amino acid, a carbohydrate, a lipid, or a hormone.

105. The method of claim 104, wherein the carbohydrate is a polysaccharide.

106. The method of claim 95, wherein the test compound is derived from a molecular library.

107. The method of claim 95, wherein the experimental cell is transfected with a nucleic acid.

108. The method of claim 107, wherein the nucleic acid encodes a TLR or a reporter construct.

109. The method of claim 108, wherein the TLR is selected from the group consisting of TLR1, TLR2, TLR3, TLR4, TLR5, TLR6, TLR7, TLR8, TLR9 and TLR10.

110. The method of claim 108, wherein the TLR is a human TLR.

111. The method of claim 108, wherein the reporter construct is selected from the group consisting of a luciferase reporter construct, a β -galactosidase reporter construct, a chloramphenicol acetyltransferase reporter construct, a green fluorescent protein reporter construct, and a secreted alkaline phosphatase construct.

112. The method of claim 111, wherein the TLR signaling activity is selected from the group consisting of luciferase expression, β -galactosidase expression, chloramphenicol acetyltransferase expression, green fluorescent protein expression, alkaline phosphatase expression and alkaline phosphatase secretion.

113. The method of claim 108, wherein the reporter construct comprises a TLR responsive promoter.

114. The method of claim 113, wherein the TLR responsive promoter
5 comprises a transcription factor binding site selected from the group consisting of an NF- κ B binding site, an AP-1 binding site, a CRE, a SRE, an ISRE, a GAS, an ATF2 binding site, an IRF3 binding site, an IRF7 binding site, an NFAT binding site, a p53 binding site, an SRF binding site, and a TARE.

115. The method of claim 113, wherein the TLR responsive promoter is a
10 promoter region selected from the group consisting of an IL-1 promoter region, an IL-6 promoter region, an IL-8 promoter region, an IL-10 promoter region, an IL-12 p40 promoter region, an IFN- α 1 promoter region, an IFN- α 4 promoter region, an IFN- β promoter region, an IFN- γ promoter region, a TNF- α promoter region, a TNF- β promoter region, an IP-9 promoter
15 region, an IP-10 promoter region, a RANTES promoter region, an ITAC promoter region, a MCP-1 promoter region, an IGFBP4 promoter region, a CD54 promoter region, a CD69 promoter region, a CD71 promoter region, a CD80 promoter region, a CD86 promoter region, a HLA-DR promoter region, and a HLA class I promoter region.

116. The method of claim 113, wherein the TLR responsive promoter is
20 selected from the group consisting of a TLR1 responsive promoter, TLR2 responsive promoter, a TLR3 responsive promoter, a TLR4 responsive promoter, a TLR5 responsive promoter, a TLR6 responsive promoter, a TLR7 responsive promoter, a TLR8 responsive promoter, a TLR9 responsive promoter and a TLR10 responsive promoter.

117. The method of claim 107, wherein the cell is stably transfected with the
25 nucleic acid.

118. The method of claim 95, wherein the TLR signaling activity is
30 measured by cytokine secretion or chemokine secretion.

119. The method of claim 118, wherein the cytokine secretion or chemokine secretion is selected from the group consisting of IL-6 secretion, IL-12 secretion and TNF- α secretion.

5 120. The method of claim 118, wherein the cytokine secretion or chemokine secretion is selected from the group consisting of IL-8 secretion, IL-10 secretion and IP-10 secretion.

10 121. The method of claim 95, wherein the TLR signaling activity is measured by phosphorylation.

122. The method of claim 121, wherein phosphorylation is total cellular phosphorylation.

15 123. The method of claim 122, wherein phosphorylation is phosphorylation of a factor selected from the group consisting of IRAK, ERK, MyD88, TRAF6, p38, NF- κ B subunits, c-Jun and c-Fos.

20 124. The method of claim 95, wherein the TLR signaling activity is measured by gene expression.

25 125. The method of claim 124, wherein the gene expression is selected from the group consisting of CD71 expression, CD86 expression, HLA-DR expression, IL-8 expression, IL-10 expression and IP-10 expression.

126. The method of claim 124, wherein the gene expression is selected from the group consisting of IL-6 expression, IL-12 expression and TNF- α expression.

30 127. The method of claim 95, wherein the TLR signaling activity is measured by microarray techniques.

128. The method of claim 95, wherein the TLR signaling activity is measured by cell proliferation.

129. The method of claim 95, wherein the TLR signaling activity is measured by cell surface marker expression.

5 130. The method of claim 129, wherein the cell surface marker expression is selected from the group consisting of CD71 cell surface expression, CD86 cell surface expression and HLA-DR MHC class II cell surface expression.

10 131. The method of claim 129, wherein the cell surface marker expression is selected from the group consisting of CD80 cell surface expression, HLA class I cell surface expression, CD54 cell surface expression and CD69 cell surface expression.

132. The method of claim 95, wherein the TLR signaling activity is measured by antibody secretion.

15 133. The method of claim 132, wherein the antibody secretion is IgM secretion.

20 134. The method of claim 95, wherein the cell is contacted to the positive reference compound and the test compound simultaneously.

135. The method of claim 95, wherein the cell is contacted to the positive reference compound prior to contact with the test compound.

25 136. The method of claim 95, wherein the cell is contacted to the test compound prior to contact with the positive reference compound.

137. A method for quality assessment of a test composition containing a known Toll like receptor (TLR) ligand, comprising:

30 measuring a reference activity of a reference composition comprising a known TLR ligand, wherein the known TLR ligand is a nucleic acid molecule;

measuring a test activity of a test composition comprising the known TLR ligand; and comparing the test activity to the reference activity.

138. The method of claim 137, further comprising selecting the test composition if the test activity falls within a predetermined range of variance about the reference activity.

139. The method of claim 1, wherein the reference composition is a first production lot of a pharmaceutical composition comprising the known TLR ligand, and wherein the test composition is a second production lot of a pharmaceutical composition comprising the known TLR ligand.

140. The method of claim 137, wherein the reference composition is a first in-process lot of a composition comprising the known TLR ligand, and wherein the test composition is a second in-process lot of a composition comprising the known TLR ligand.

141. The method of claim 137, wherein the measuring the reference activity comprises contacting the reference composition with an isolated cell expressing a TLR responsive to the known TLR ligand, and wherein the measuring the test activity comprises contacting the test composition with the isolated cell expressing a TLR responsive to the known TLR ligand.

142. The method of claim 141, wherein the isolated cell expressing the TLR responsive to the known TLR ligand comprises an expression vector for the TLR responsive to the known TLR ligand.

143. The method of claim 141, wherein the isolated cell expressing the TLR responsive to the known TLR ligand naturally expresses the TLR responsive to the known TLR ligand.

144. The method of claim 141, wherein the isolated cell expressing the TLR responsive to the known TLR ligand is RPMI 8226.

145. The method of claim 137, wherein the measuring the reference activity and the measuring the test activity each comprise measuring signaling activity mediated by a TLR responsive to the known TLR ligand.

5 146. The method of claim 145, wherein the signaling activity is activity of a reporter construct under control of NF- κ B response element.

147. The method of claim 145, wherein the signaling activity is activity of a reporter construct under control of interferon-stimulated response element (ISRE).

10

148. The method of claim 145, wherein the signaling activity is activity of a reporter gene under control of an IFN- α promoter.

149. The method of claim 145, wherein the signaling activity is activity of a
15 reporter gene under control of an IFN- β promoter.

150. The method of claim 145, wherein the signaling activity is activity of a reporter gene under control of an IL-6 promoter.

20 151. The method of claim 145, wherein the signaling activity is activity of a reporter gene under control of an IL-8 promoter.

152. The method of claim 145, wherein the signaling activity is activity of a reporter gene under control of an IL-12 p40 promoter.

25

153. The method of claim 145, wherein the signaling activity is activity of a reporter gene under control of a RANTES promoter.

154. The method of claim 137, wherein the known TLR ligand is a TLR9
30 ligand.

155. The method of claim 137, wherein the known TLR ligand is a TLR3 ligand.

156. The method of claim 137, wherein the known TLR ligand is a TLR7 ligand.

5 157. The method of claim 137, wherein the known TLR ligand is a TLR8 ligand.

158. The method of claim 137, wherein the known TLR ligand is an immunostimulatory nucleic acid.

10 159. The method of claim 137, wherein the known TLR ligand is a CpG nucleic acid.

15 160. The method of claim 137, wherein the known TLR ligand is an immunoinhibitory nucleic acid.

161. A method for quality assessment of a test lot of a pharmaceutical product containing a known TLR9 ligand, comprising:

20 measuring a reference activity of a reference lot of a pharmaceutical product comprising a known TLR9 ligand, wherein the known TLR9 ligand is a nucleic acid molecule;

measuring a test activity of a test lot of a pharmaceutical product comprising the known TLR9 ligand;

comparing the test activity to the reference activity; and

25 rejecting the test lot if the test activity falls outside of a predetermined range of variance about the reference activity.

162. The method of claim 161, wherein the known TLR9 ligand is an oligonucleotide comprising a base sequence TCGTCGTTTTGTCGTTTTGTCGTT (SEQ ID
30 NO:1).

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163. The method of claim 161, wherein the known TLR9 ligand is an oligonucleotide comprising a base sequence 5'-TCGTCGTTTTGACGTTTTGTCGTT-3' (SEQ ID NO:139).

5 164. The method of claim 161, wherein the known TLR9 ligand is an oligonucleotide comprising a base sequence 5'-TCGTCGTTTTGTCGTTTTTTTCGA-3' (SEQ ID NO:140).

10 165. The method of claim 161, wherein the known TLR9 ligand is an oligonucleotide comprising a base sequence 5'-TCGTCGTTTCGTCGTTTCGTCGTT-3' (SEQ ID NO:141).

15 166. The method of claim 161, wherein the known TLR9 ligand is an oligonucleotide comprising a base sequence 5'-TCGTCGTTTCGTCGTTTTGTCGTT-3' (SEQ ID NO:142).

20 167. The method of claim 161, wherein the known TLR9 ligand is an oligonucleotide comprising a base sequence 5'-TCGTCGTTTTTCGGTCGTTTT-3' (SEQ ID NO:143).

168. The method of claim 161, wherein the known TLR9 ligand is an oligonucleotide comprising a base sequence 5'-TCGTCGTTTTTCGTGCGTTTT-3' (SEQ ID NO:144).

25 169. The method of claim 161, wherein the known TLR9 ligand is an oligonucleotide comprising a base sequence 5'-TCGTCGTTTTCGGCGGCCGCG-3' (SEQ ID NO:145).

30 170. The method of claim 161, wherein the known TLR9 ligand is an oligonucleotide comprising a base sequence 5'-TCGTC_GTTTTAC_GGCGCC_GTGCCG-3' (SEQ ID NO:146), wherein every internucleoside linkage is phosphorothioate except for those indicated by “_”, which are phosphodiester.

171. A screening method for identifying agonists of Toll-like receptor (TLR) signaling activity, comprising

contacting a cell that expresses a TLR with a test compound and measuring a test level of TLR signaling activity,

5 wherein a test level that is positive is indicative of a test compound that is a TLR agonist, and

wherein the cell is a Raji cell, a RAMOS cell, a Nalm cell, a THP-1 cell, or a KG-1 cell, and the TLR is TLR9.

10 172. A screening method for identifying agonists of Toll-like receptor (TLR) signaling activity, comprising

contacting a cell that expresses a TLR with a test compound and measuring a test level of TLR signaling activity,

15 wherein a test level that is positive is indicative of a test compound that is a TLR agonist, and

wherein the cell is a Raji cell or a RAMOS cell, and the TLR is TLR7.

173. A screening method for identifying agonists of Toll-like receptor (TLR) signaling activity, comprising

20 contacting a cell that expresses a TLR with a test compound and measuring a test level of TLR signaling activity,

wherein a test level that is positive is indicative of a test compound that is a TLR agonist, and

25 wherein the cell is a Raji cell, a RAMOS cell, a KG-1 cell, a Nalm-6 cell, a Jurkat cell, a Hela cell, a Hep-2 cell, an A549 cell, a Bewo cell, an NK-92 cell or an NK-92 MI cell, and the TLR is TLR3.

174. A screening method for identifying antagonists of Toll-like receptor (TLR) signaling activity, comprising

30 contacting a cell with a positive reference compound and measuring a reference level of TLR signaling activity,

contacting the cell with the positive reference compound and a test compound, and measuring a test level of TLR signaling activity,

wherein a test level that is less than a reference level is indicative of a test compound that is a TLR antagonist, and

wherein the cell is selected from the group consisting of a RPMI 8226 cell, a RAMOS cell, a Raji cell, a THP-1 cell, a Nalm cell and a KG-1 cell, and the TLR is TLR9.

5

175. A screening method for identifying antagonists of Toll-like receptor (TLR) signaling activity, comprising

contacting a cell with a positive reference compound and measuring a reference level of TLR signaling activity,

10

contacting the cell with the positive reference compound and a test compound, and measuring a test level of TLR signaling activity,

wherein a test level that is less than a reference level is indicative of a test compound that is a TLR antagonist, and

wherein the cell is selected from the group consisting of a RPMI 8226 cell, a RAMOS cell and a Raji cell, and the TLR is TLR7.

15

175. A screening method for identifying antagonists of Toll-like receptor (TLR) signaling activity, comprising

contacting a cell with a positive reference compound and measuring a reference level of TLR signaling activity,

20

contacting the cell with the positive reference compound and a test compound, and measuring a test level of TLR signaling activity,

wherein a test level that is less than a reference level is indicative of a test compound that is a TLR antagonist, and

25

wherein the cell is selected from the group consisting of a Raji cell, a RAMOS cell, a KG-1 cell, a Nalm-6 cell, a Jurkat cell, a Hela cell, a Hep-2 cell, an A549 cell, a Bewo cell, an NK-92 cell and an NK-92 MI cell, and the TLR is TLR3.

176. A screening method for identifying an enhancer of a Toll-like receptor (TLR) agonist, comprising

30

contacting a cell with a positive reference compound and measuring a reference level of TLR signaling activity, and

contacting a cell with the positive reference compound and a test compound and measuring a test level of TLR signaling activity,

wherein the positive reference compound is a TLR agonist, and a test level that is greater than the reference level is indicative of a test compound that is an enhancer of a TLR agonist.

177. The method of claim 176, wherein the positive reference compound is an immunostimulatory nucleic acid.

178. The method of claim 176, wherein the positive reference compound is an imidazoquinoline compound.

180. The method of claim 176, wherein the cell is selected from the group consisting of a KG-1 cell, a Nalm-6 cell, a Raji cell, a RAMOS cell, a Jurkat cell, a Hela cell, a Hep-2 cell, an A549 cell, a Bewo cell, an NK-92 cell and an NK-92 MI cell, and the TLR is TLR3.

181. The method of claim 176, wherein the cell is selected from the group consisting of a KG-1 cell, a Nalm-6 cell, a Raji cell, an RPMI 8226 cell, a RAMOS cell, and a THP-1 cell, and the TLR is TLR9.

182. The method of claim 176, wherein the cell is selected from the group consisting of a Raji cell, an RPMI 8226 cell and a RAMOS cell, and the TLR is TLR7.

183. The method of claim 1, wherein the TLR is TLR7 or TLR9.

184. The method of claim 172-175 or 176, wherein the cell is unmodified.

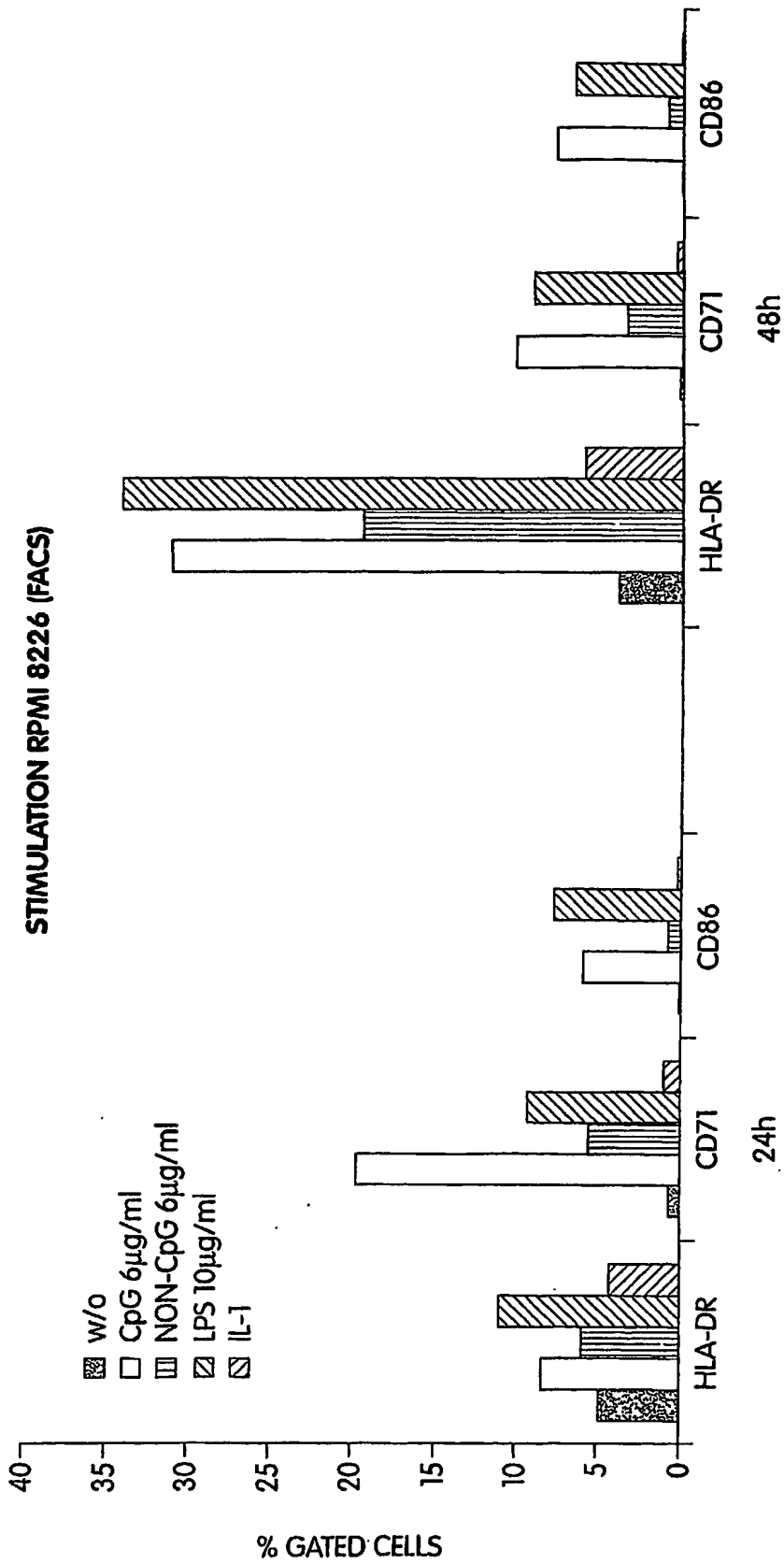


Fig. 1

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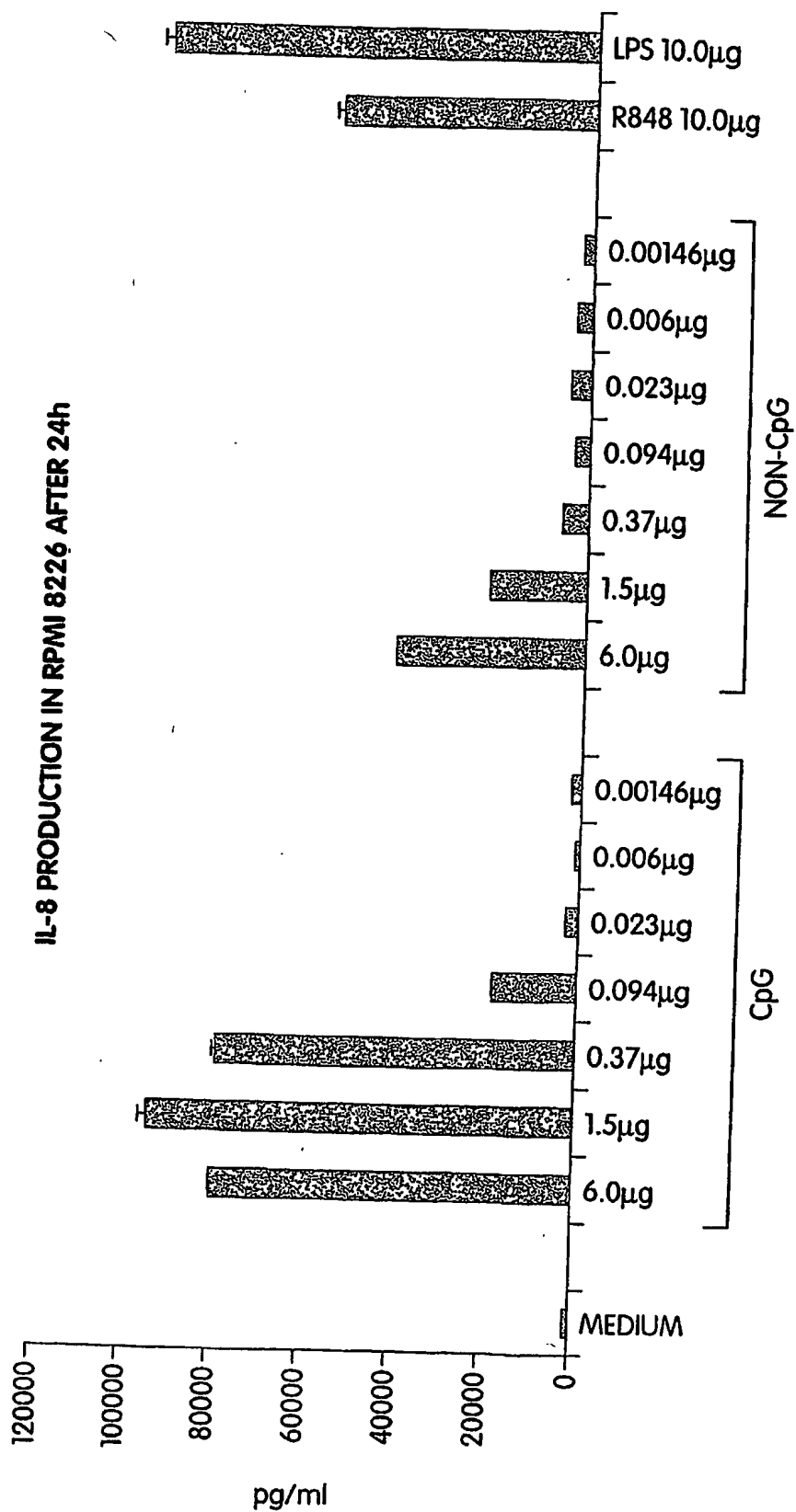


Fig. 2

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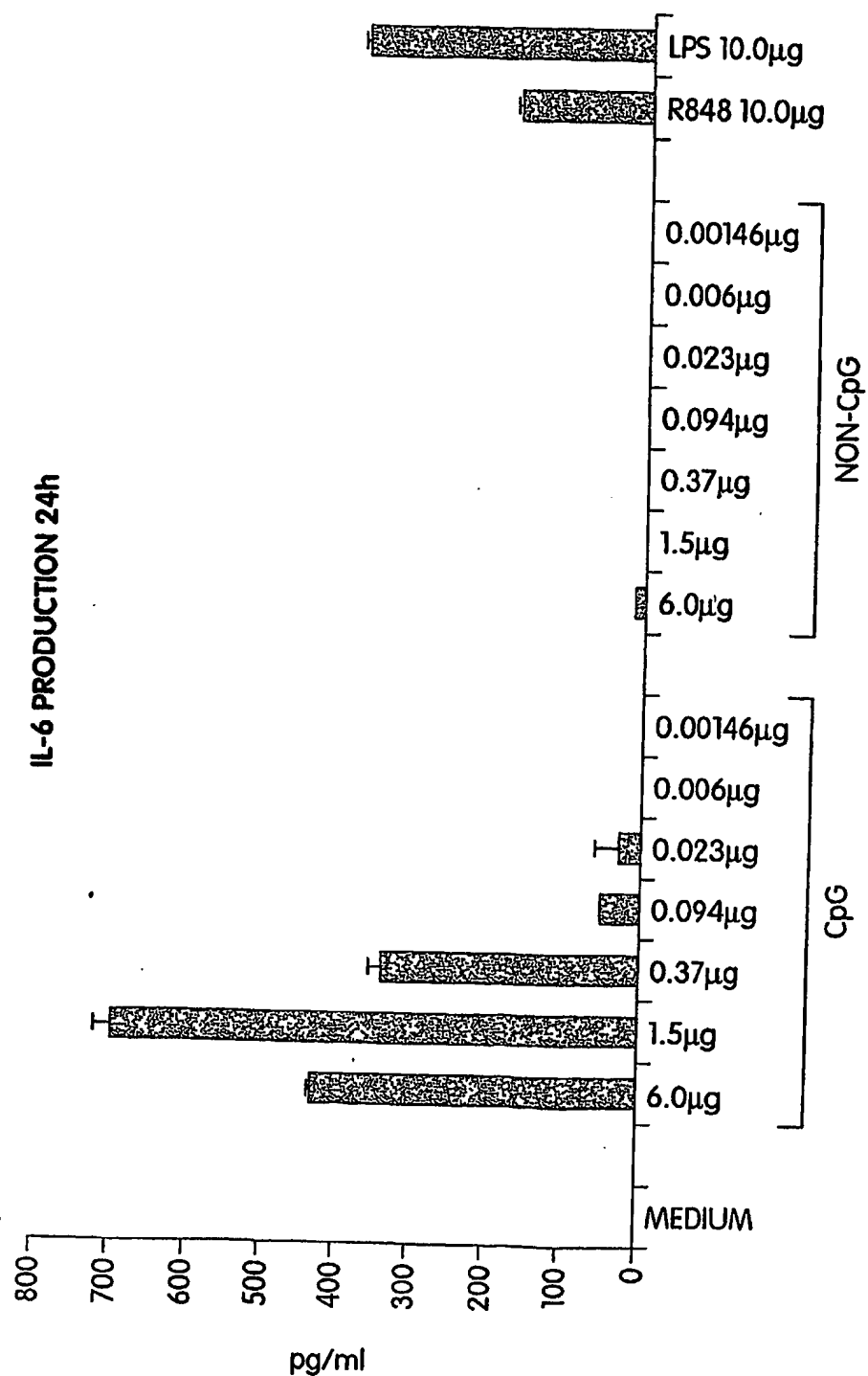


Fig. 3

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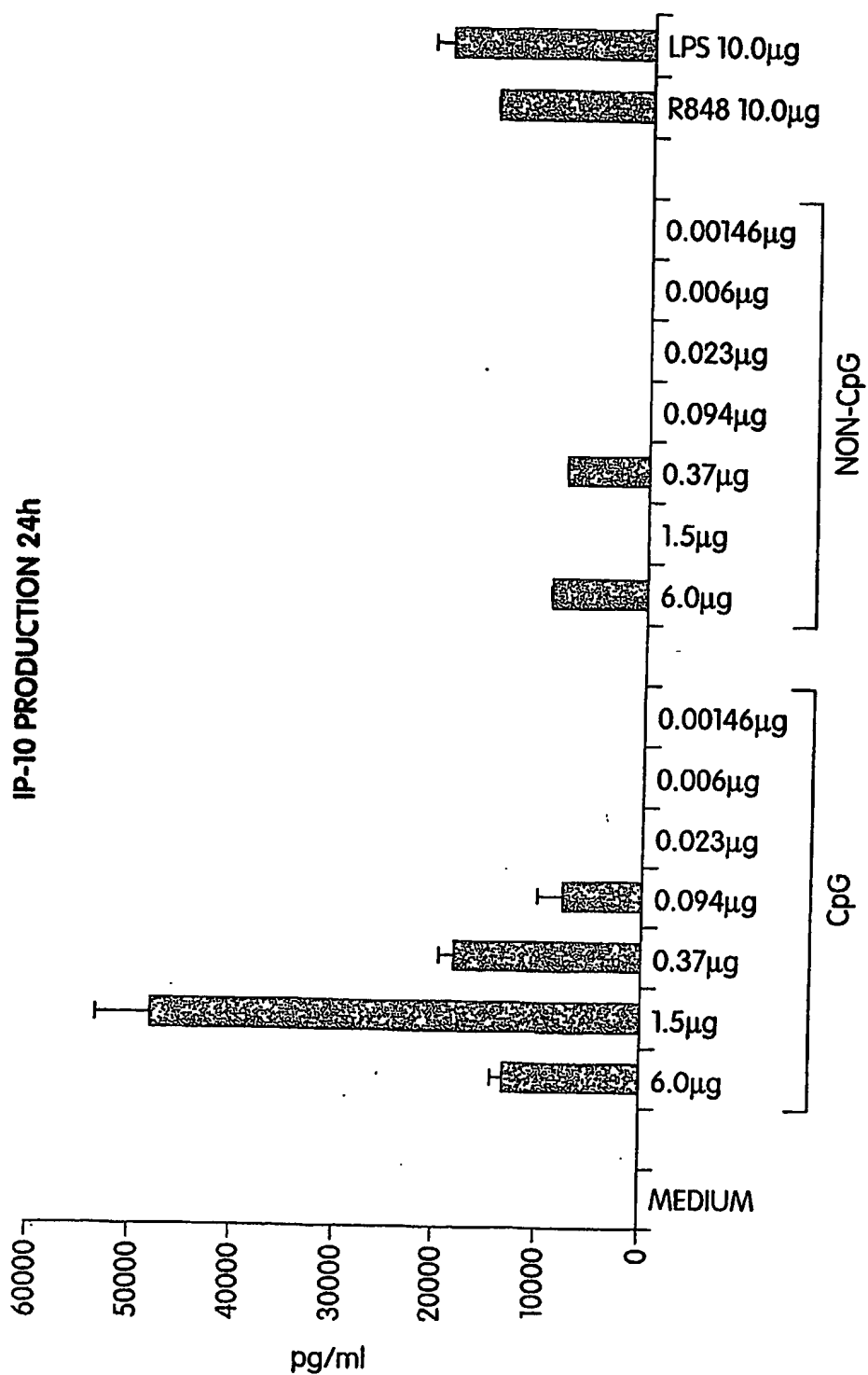


Fig. 4

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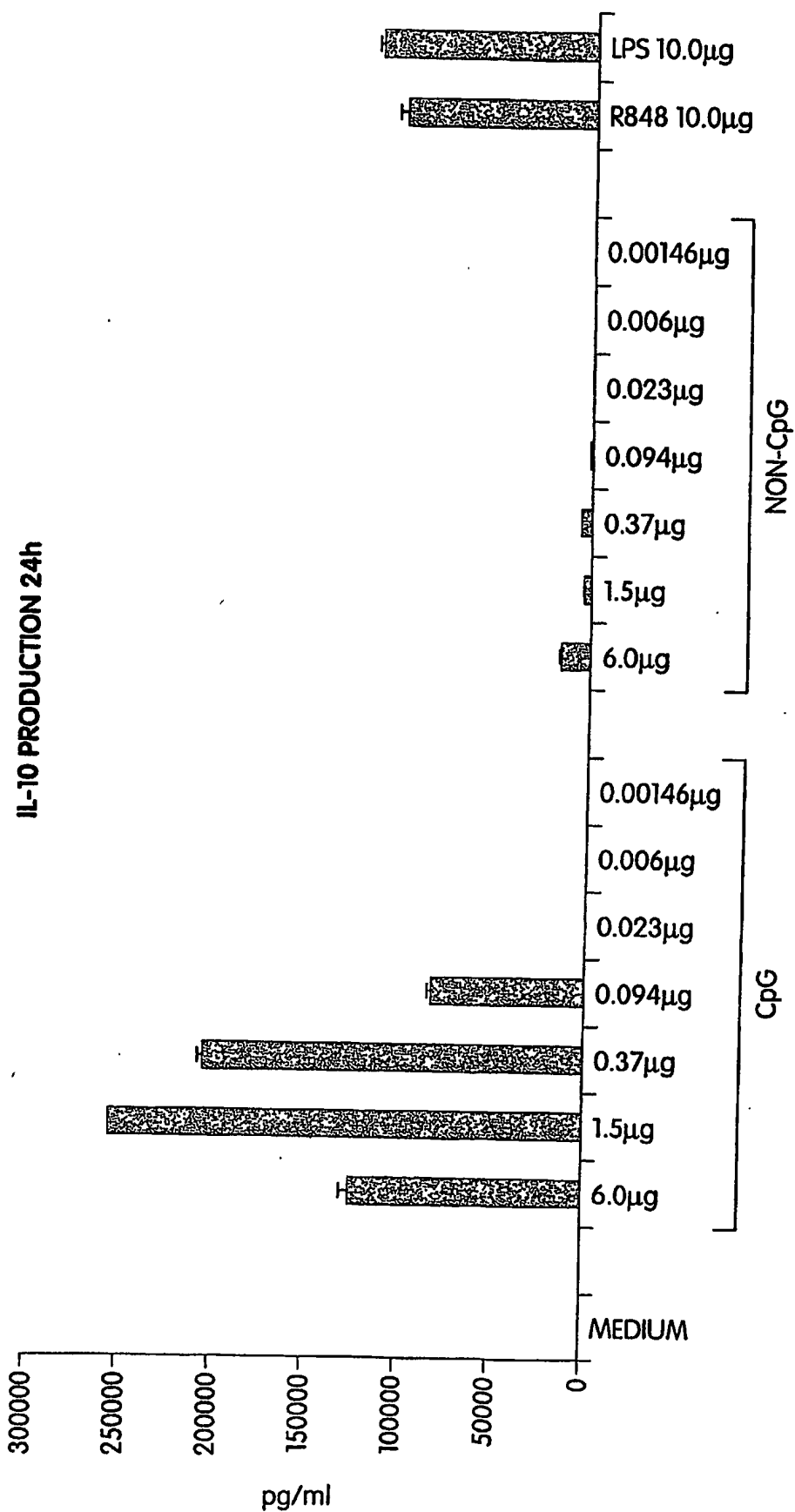
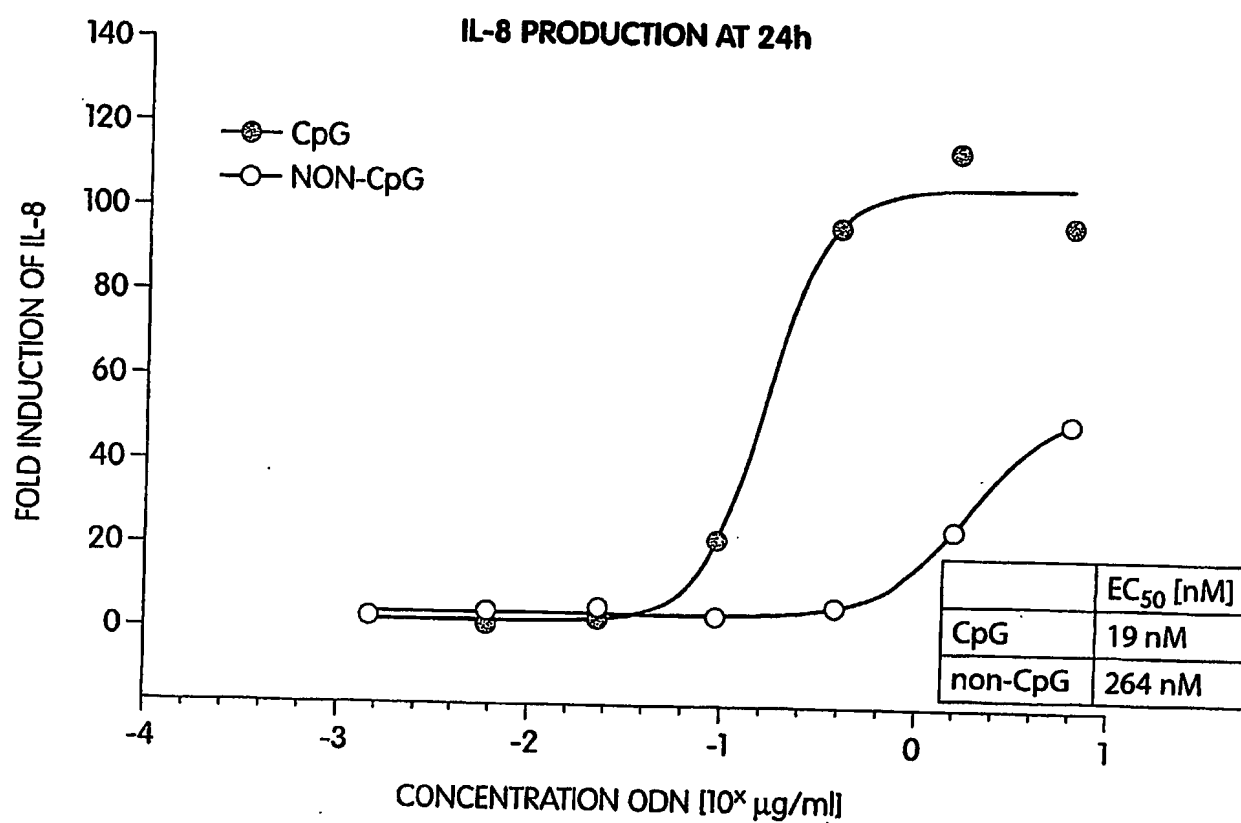


Fig. 5

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**Fig. 6**

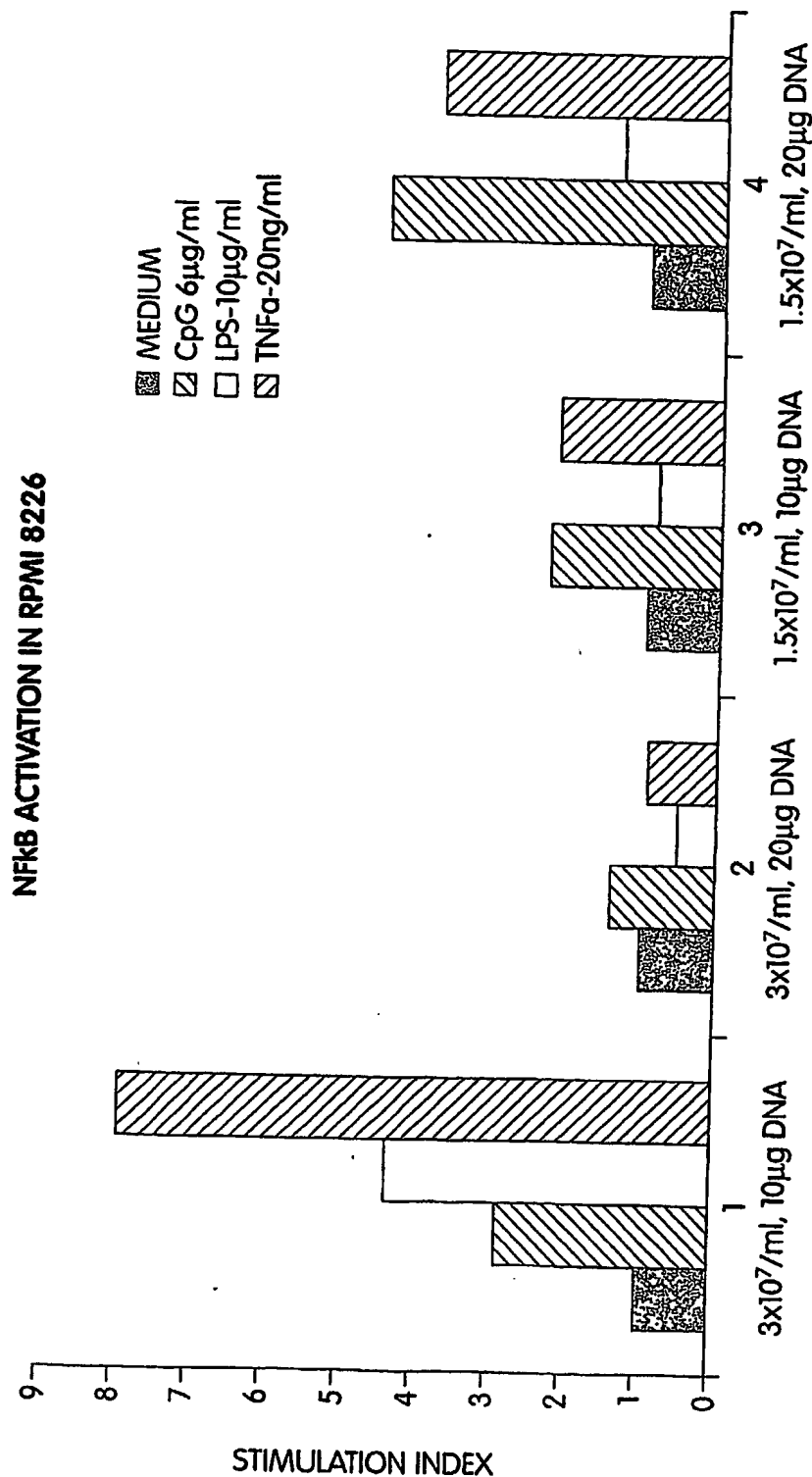


Fig. 7

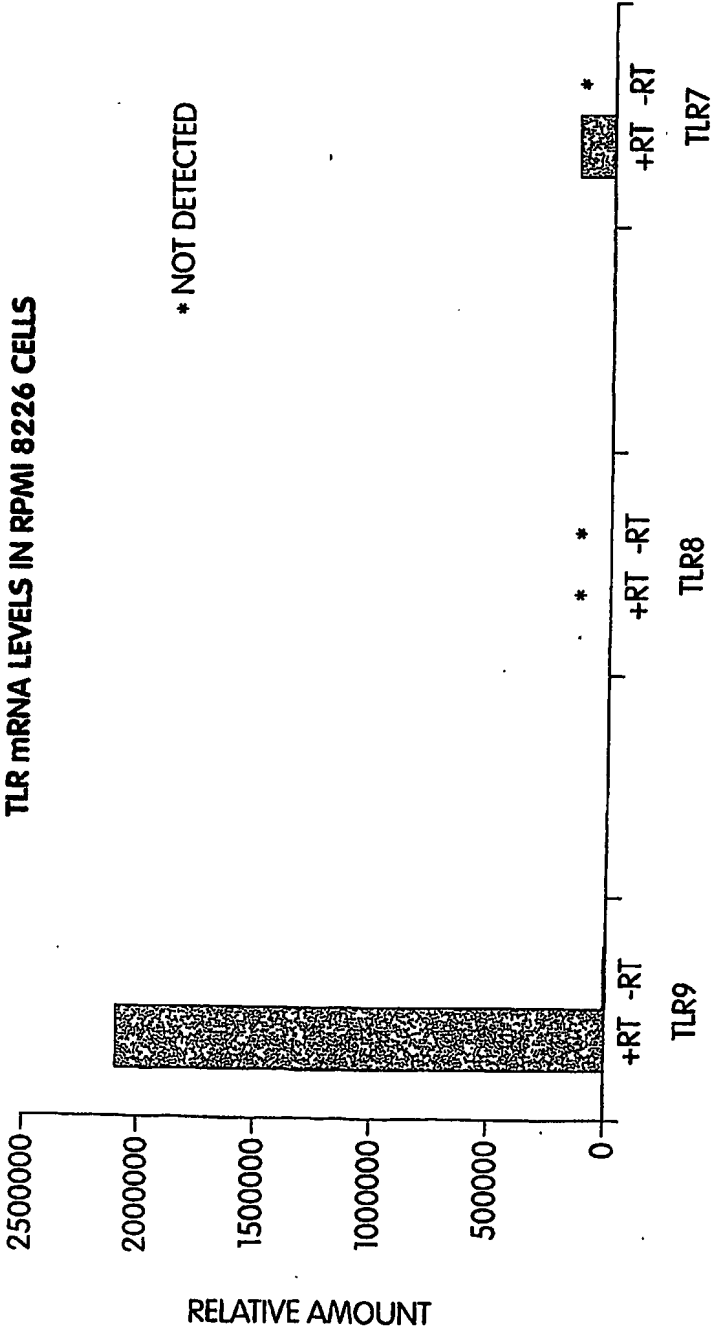


Fig. 8

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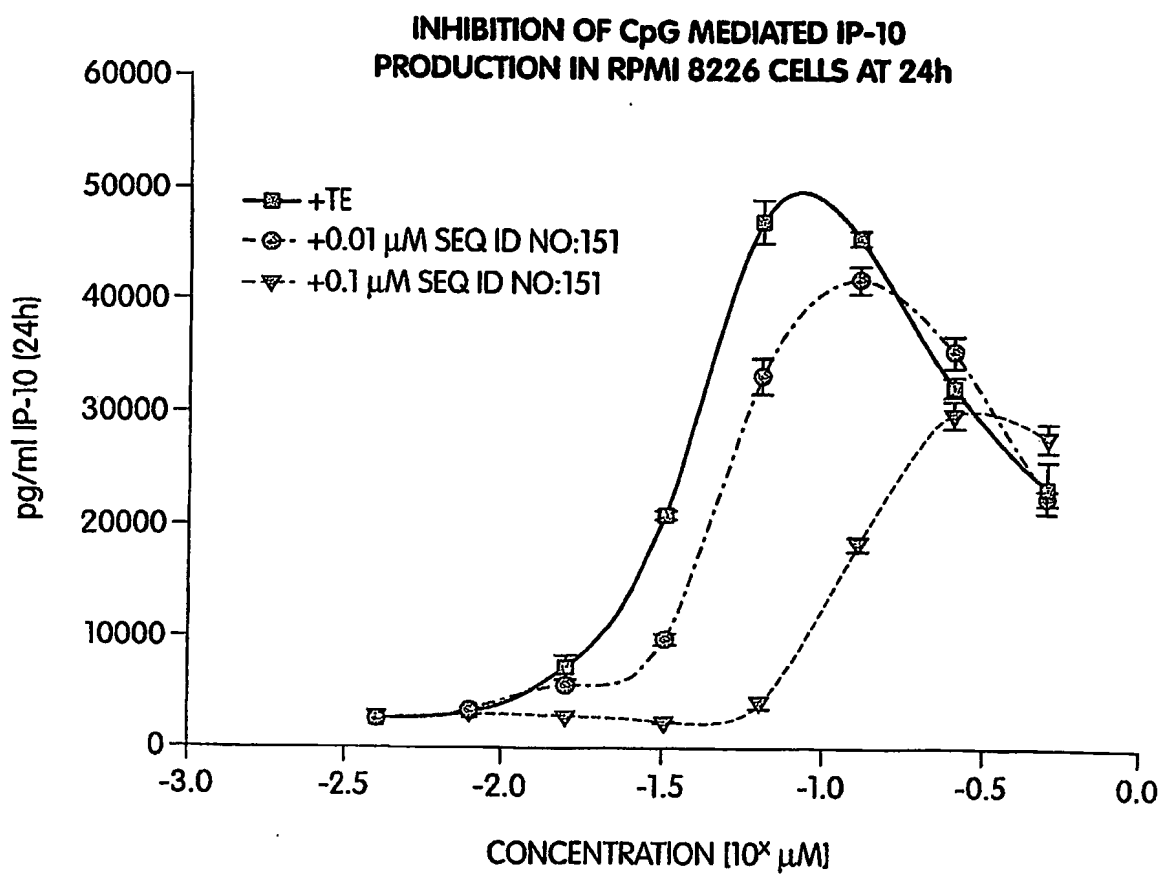


Fig. 9

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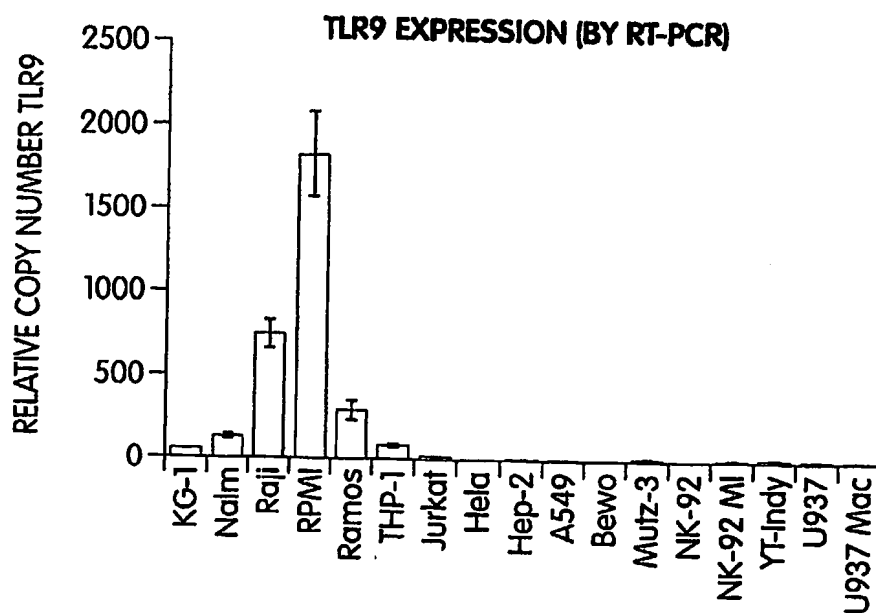


Fig. 10

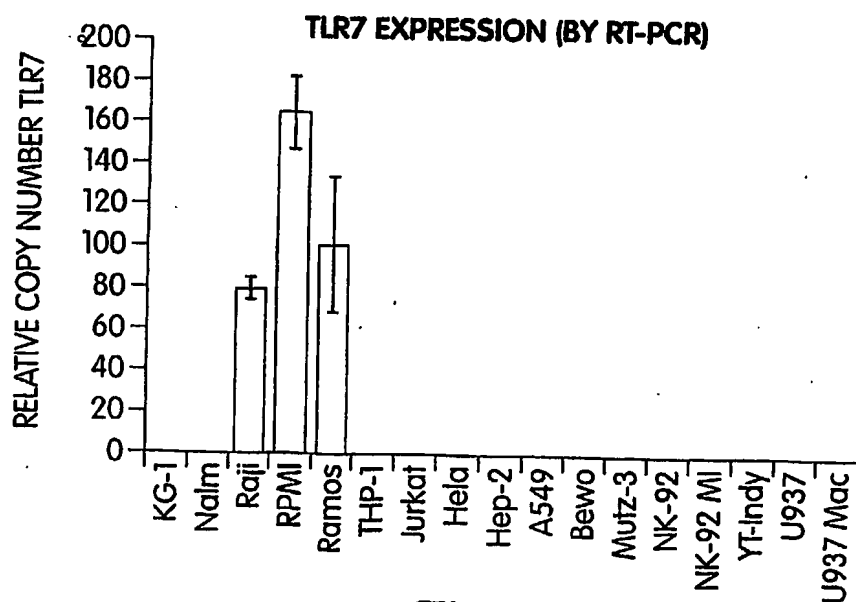


Fig. 11

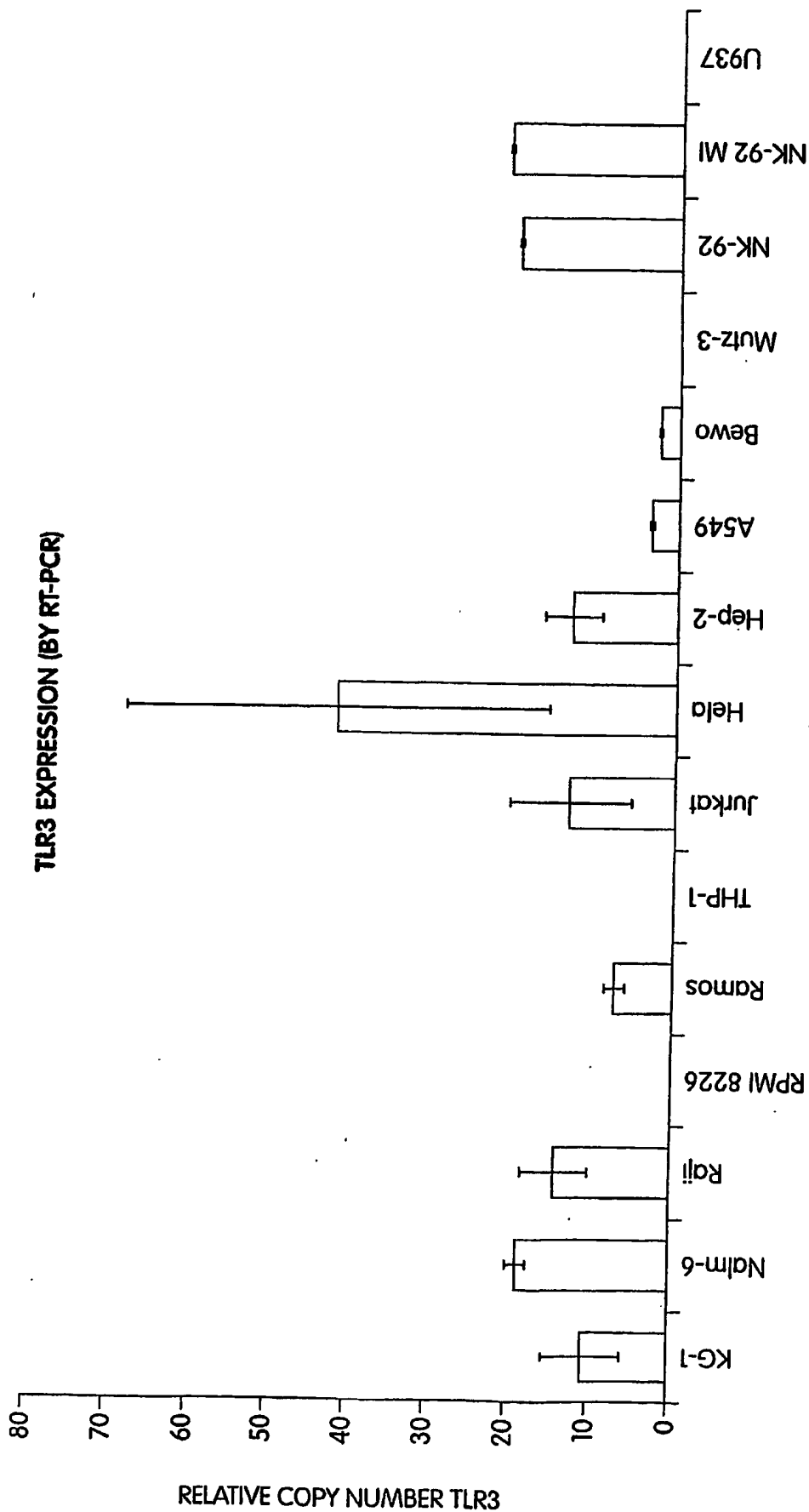


Fig. 12

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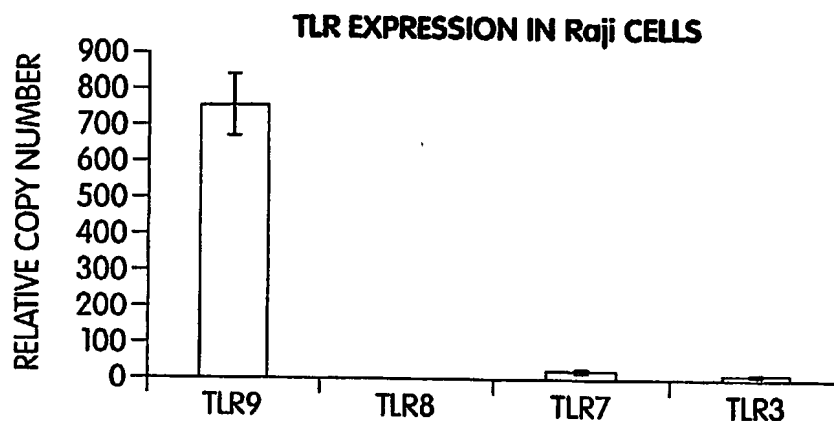


Fig. 13

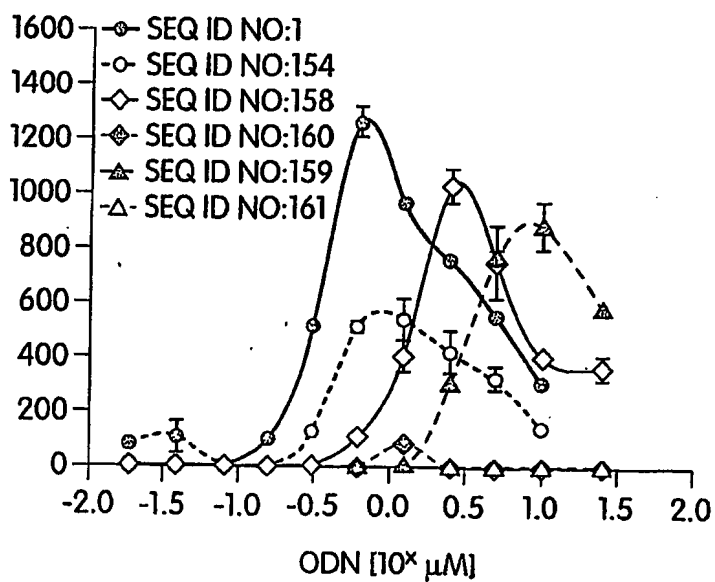


Fig. 14

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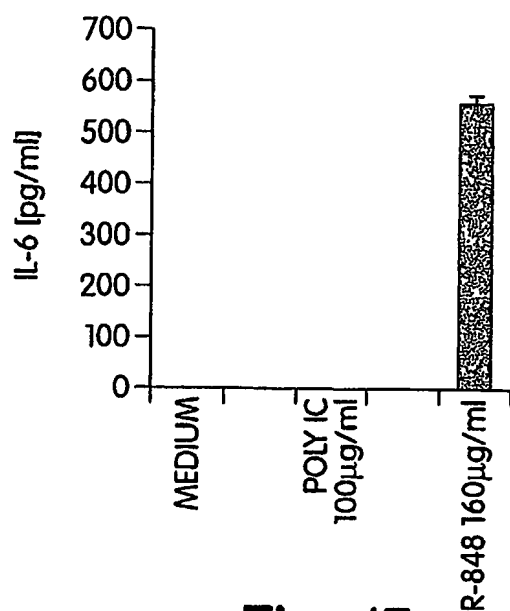


Fig. 15

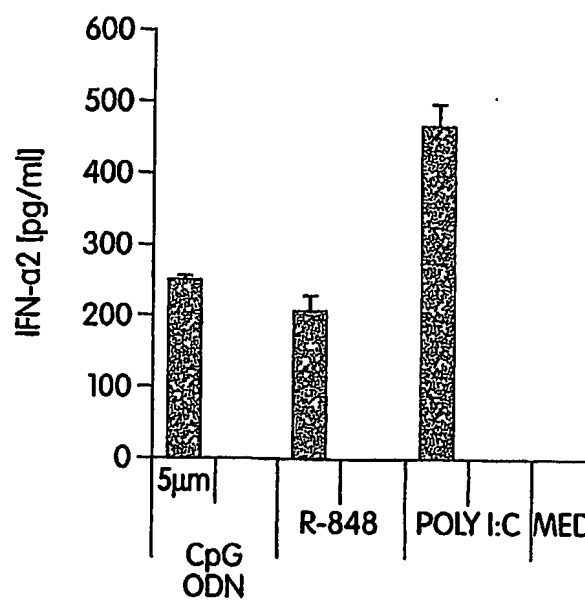


Fig. 16

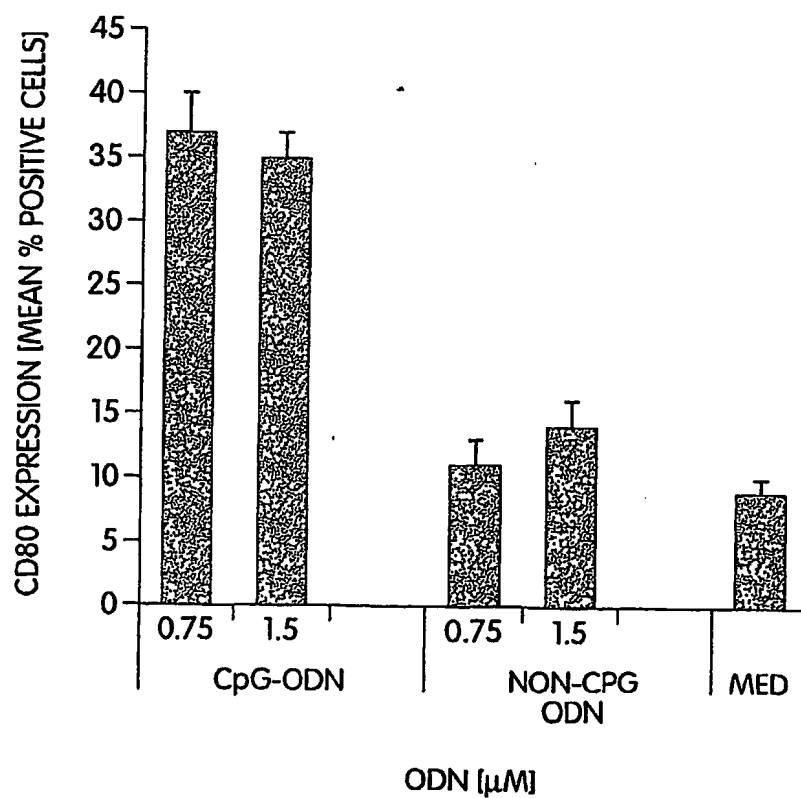


Fig. 17

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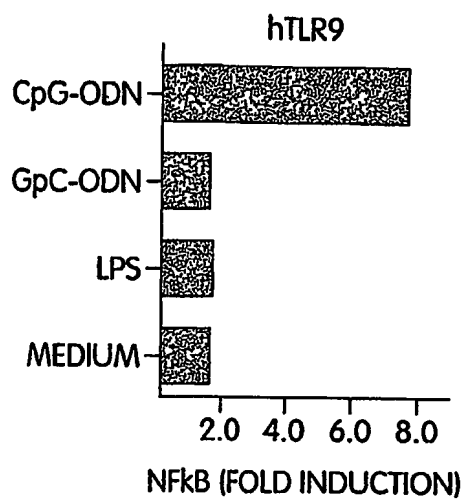


Fig. 18A

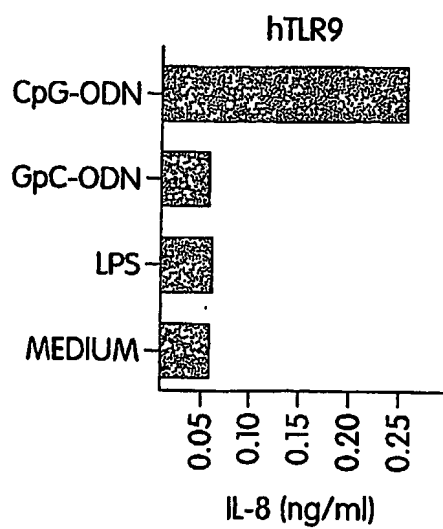
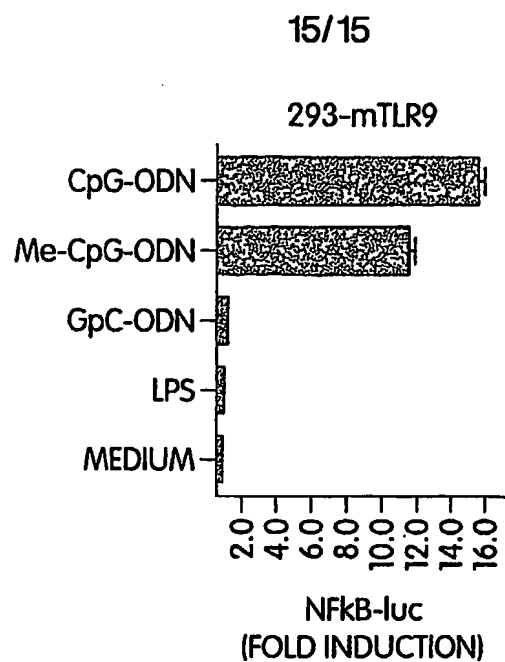
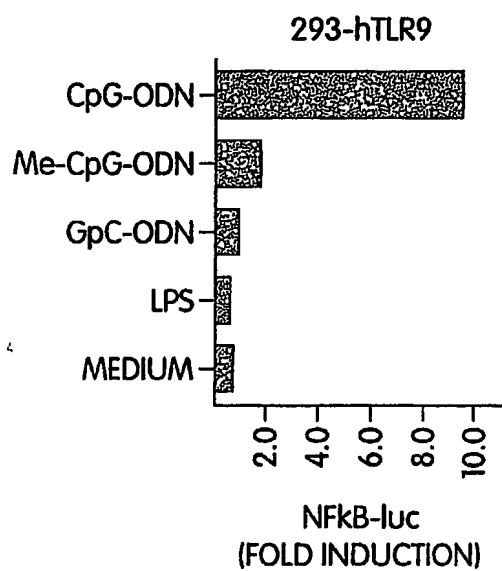
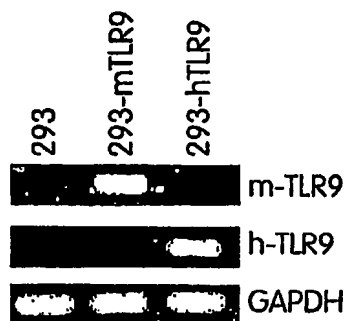


Fig. 18B

**Fig. 19****Fig. 20****Fig. 21**

SEQUENCE LISTING

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COLEY PHARMACEUTICAL GROUP INC.

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<212> PRT

<213> Homo sapiens

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Asn Gly Ile Cys Lys Gly Ser Ser Gly Ser Leu Asn Ser Ile Pro Ser
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Gly Leu Thr Glu Ala Val Lys Ser Leu Asp Leu Ser Asn Asn Arg Ile
          50           55           60

Thr Tyr Ile Ser Asn Ser Asp Leu Gln Arg Cys Val Asn Leu Gln Ala
65           70           75           80

Leu Val Leu Thr Ser Asn Gly Ile Asn Thr Ile Glu Glu Asp Ser Phe
          85           90           95

Ser Ser Leu Gly Ser Leu Glu His Leu Asp Leu Ser Tyr Asn Tyr Leu
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Ser Asn Leu Ser Ser Ser Trp Phe Lys Pro Leu Ser Ser Leu Thr Phe
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Thr Phe Thr Lys Ile Gln Arg Lys Asp Phe Ala Gly Leu Thr Phe Leu
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Glu Glu Leu Glu Ile Asp Ala Ser Asp Leu Gln Ser Tyr Glu Pro Lys
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Asn Tyr Leu Cys Asp Ser Pro Ser His Val Arg Gly Gln Gln Val Gln		
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Asp Val Arg Leu Ser Val Ser Glu Cys His Arg Thr Ala Leu Val Ser		
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Gly Met Cys Cys Ala Leu Phe Leu Leu Ile Leu Leu Thr Gly Val Leu		
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Cys His Arg Phe His Gly Leu Trp Tyr Met Lys Met Met Trp Ala Trp		
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Tyr Asp Ala Phe Val Ser Tyr Ser Glu Arg Asp Ala Tyr Trp Val Glu		
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Cys Leu His Lys Arg Asp Phe Ile Pro Gly Lys Trp Ile Ile Asp Asn		
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His Phe Arg Leu Phe Glu Glu Asn Asn Asp Ala Ala Ile Leu Ile Leu		
725	730	735
Leu Glu Pro Ile Glu Lys Lys Ala Ile Pro Gln Arg Phe Cys Lys Leu		
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Arg Lys Ile Met Asn Thr Lys Thr Tyr Leu Glu Trp Pro Met Asp Glu		
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Ser Gly Val Cys Asp Gly Arg Ser Arg Ser Phe Thr Ser Ile Pro Ser
          35          40          45

Gly Leu Thr Ala Ala Met Lys Ser Leu Asp Leu Ser Phe Asn Lys Ile
50          55          60

Thr Tyr Ile Gly His Gly Asp Leu Arg Ala Cys Ala Asn Leu Gln Val
65          70          75          80

Leu Ile Leu Lys Ser Ser Arg Ile Asn Thr Ile Glu Gly Asp Ala Phe
          85          90          95

Tyr Ser Leu Gly Ser Leu Glu His Leu Asp Leu Ser Asp Asn His Leu
100          105          110

Ser Ser Leu Ser Ser Ser Trp Phe Gly Pro Leu Ser Ser Leu Lys Tyr
115          120          125

Leu Asn Leu Met Gly Asn Pro Tyr Gln Thr Leu Gly Val Thr Ser Leu
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Thr Phe Ser Lys Asp Gln Leu Gly Ser Phe Pro Lys Leu Glu Thr Leu						
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Glu Ala Gly Asp Asn His Phe Val Cys Ser Cys Glu Leu Leu Ser Phe						
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Thr Met Glu Thr Pro Ala Leu Ala Gln Ile Leu Val Asp Trp Pro Asp						
	545		550		555	560
Ser Tyr Leu Cys Asp Ser Pro Pro Arg Leu His Gly His Arg Leu Gln						
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Asp Ala Arg Pro Ser Val Leu Glu Cys His Gln Ala Ala Leu Val Ser						
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Gly Val Cys Cys Ala Leu Leu Leu Leu Ile Leu Leu Val Gly Ala Leu						
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Cys His His Phe His Gly Leu Trp Tyr Leu Arg Met Met Trp Ala Trp						
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Leu Gln Ala Lys Arg Lys Pro Lys Lys Ala Pro Cys Arg Asp Val Cys						
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Tyr Asp Ala Phe Val Ser Tyr Ser Glu Gln Asp Ser His Trp Val Glu						
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Asn Leu Met Val Gln Gln Leu Glu Asn Ser Asp Pro Pro Phe Lys Leu						
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Cys Leu His Lys Arg Asp Phe Val Pro Gly Lys Trp Ile Ile Asp Asn						
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Ile Ile Asp Ser Ile Glu Lys Ser His Lys Thr Val Phe Val Leu Ser						
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His Phe Arg Leu Phe Asp Glu Asn Asn Asp Ala Ala Ile Leu Val Leu						
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Leu Glu Pro Ile Glu Arg Lys Ala Ile Pro Gln Arg Phe Cys Lys Leu						
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Arg Lys Ile Met Asn Thr Lys Thr Tyr Leu Glu Trp Pro Leu Asp Glu						
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Arg Leu Pro Ala Ala Asn Phe Thr Arg Tyr Ser Gln Leu Thr Ser Leu

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Arg Arg Leu Pro Pro Thr Asn Phe Thr Arg Tyr Ser Gln Leu Ala Ile
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ctgttgtagc	agttctggtc	tataagttct	attttcacct	gatgcttctt	gctggctgca	2280
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aaggtttcca	taaaagccga	aagggtgattg	ttgtggtgtc	ccagcacttc	atccagagcc	2520
gctgggtgat	ctttgaatat	gagattgctc	agacctggca	gtttctgagc	agtcgtgctg	2580
gtatcatctt	cattgtcctg	cagaaggtgg	agaagaccct	gctcaggcag	caggtggagc	2640
tgtaccgcct	tctcagcagg	aacacttacc	tggagtggga	ggacagtgtc	ctggggcggc	2700
acatcttctg	gagacgactc	agaaaagccc	tgctggatgg	taaatcatgg	aatccagaag	2760
gaacagtggg	tacaggatgc	aattggcagg	aagcaacatc	tatctgaaga	ggaaaaataa	2820
aaacctcctg	aggcatttct	tgcccagctg	ggccaacac	ttgttcagtt	aataagtatt	2880

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aaatgctgcc acatgtcagg ccttatgcta agggtagagta attccatggg gcactagata 2940
tgcagggctg ctaatctcaa ggagcttcca gtgcagaggg aataaatgct agactaaaat 3000
acagagtott ccagggtgggc atttcaacca actcagtcaa ggaacccatg acaaagaaag 3060
tcatttcaac tcttacctca tcaagttgaa taaagacaga gaaaacagaa agagacattg 3120
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ttggtagttt tgactgaact ggggtgttcac tttttccttt ttgattgaat acaattttaa 3240
ttctacttga tgactgcagt cgtcaagggg ctctgatgc aagatgcccc ttccatttta 3300
agtctgtctc cttacagagg ttaaagtcta gtggctaatt cctaaggaaa cctgattaac 3360
acatgctcac aaccatcctg gtcattctcg agcatgttct attttttaac taatcacccc 3420
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gcctactaag taatgactgt catgaaagca gcattgaaat aatttgttta aagggggcac 3660
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ggctgataaa cccggggtga cctcatgaaa tgagttgcag cagaagtta tttttttcag 3840
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<210> 16

<211> 839

<212> PRT

<213> Homo sapiens

<400> 16

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Met Met Ser Ala Ser Arg Leu Ala Gly Thr Leu Ile Pro Ala Met Ala
1             5             10             15

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Phe Leu Ser Cys Val Arg Pro Glu Ser Trp Glu Pro Cys Val Glu Val
20             25             30

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```

Val Pro Asn Ile Thr Tyr Gln Cys Met Glu Leu Asn Phe Tyr Lys Ile
35             40             45

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```

Pro Asp Asn Leu Pro Phe Ser Thr Lys Asn Leu Asp Leu Ser Phe Asn
50             55             60

```

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Pro Leu Arg His Leu Gly Ser Tyr Ser Phe Phe Ser Phe Pro Glu Leu
65             70             75             80

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Gln Val Leu Asp Leu Ser Arg Cys Glu Ile Gln Thr Ile Glu Asp Gly
85             90             95

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Ala Tyr Gln Ser Leu Ser His Leu Ser Thr Leu Ile Leu Thr Gly Asn
 100 105 110
 Pro Ile Gln Ser Leu Ala Leu Gly Ala Phe Ser Gly Leu Ser Ser Leu
 115 120 125
 Gln Lys Leu Val Ala Val Glu Thr Asn Leu Ala Ser Leu Glu Asn Phe
 130 135 140
 Pro Ile Gly His Leu Lys Thr Leu Lys Glu Leu Asn Val Ala His Asn
 145 150 155 160
 Leu Ile Gln Ser Phe Lys Leu Pro Glu Tyr Phe Ser Asn Leu Thr Asn
 165 170 175
 Leu Glu His Leu Asp Leu Ser Ser Asn Lys Ile Gln Ser Ile Tyr Cys
 180 185 190
 Thr Asp Leu Arg Val Leu His Gln Met Pro Leu Leu Asn Leu Ser Leu
 195 200 205
 Asp Leu Ser Leu Asn Pro Met Asn Phe Ile Gln Pro Gly Ala Phe Lys
 210 215 220
 Glu Ile Arg Leu His Lys Leu Thr Leu Arg Asn Asn Phe Asp Ser Leu
 225 230 235 240
 Asn Val Met Lys Thr Cys Ile Gln Gly Leu Ala Gly Leu Glu Val His
 245 250 255
 Arg Leu Val Leu Gly Glu Phe Arg Asn Glu Gly Asn Leu Glu Lys Phe
 260 265 270
 Asp Lys Ser Ala Leu Glu Gly Leu Cys Asn Leu Thr Ile Glu Glu Phe
 275 280 285
 Arg Leu Ala Tyr Leu Asp Tyr Tyr Leu Asp Asp Ile Ile Asp Leu Phe
 290 295 300
 Asn Cys Leu Thr Asn Val Ser Ser Phe Ser Leu Val Ser Val Thr Ile
 305 310 315 320
 Glu Arg Val Lys Asp Phe Ser Tyr Asn Phe Gly Trp Gln His Leu Glu
 325 330 335
 Leu Val Asn Cys Lys Phe Gly Gln Phe Pro Thr Leu Lys Leu Lys Ser
 340 345 350
 Leu Lys Arg Leu Thr Phe Thr Ser Asn Lys Gly Gly Asn Ala Phe Ser
 355 360 365
 Glu Val Asp Leu Pro Ser Leu Glu Phe Leu Asp Leu Ser Arg Asn Gly
 370 375 380
 Leu Ser Phe Lys Gly Cys Cys Ser Gln Ser Asp Phe Gly Thr Thr Ser
 385 390 395 400
 Leu Lys Tyr Leu Asp Leu Ser Phe Asn Gly Val Ile Thr Met Ser Ser
 405 410 415
 Asn Phe Leu Gly Leu Glu Gln Leu Glu His Leu Asp Phe Gln His Ser

			420					425					430			
Asn	Leu	Lys	Gln	Met	Ser	Glu	Phe	Ser	Val	Phe	Leu	Ser	Leu	Arg	Asn	
		435					440					445				
Leu	Ile	Tyr	Leu	Asp	Ile	Ser	His	Thr	His	Thr	Arg	Val	Ala	Phe	Asn	
	450					455					460					
Gly	Ile	Phe	Asn	Gly	Leu	Ser	Ser	Leu	Glu	Val	Leu	Lys	Met	Ala	Gly	
465					470					475					480	
Asn	Ser	Phe	Gln	Glu	Asn	Phe	Leu	Pro	Asp	Ile	Phe	Thr	Glu	Leu	Arg	
				485					490					495		
Asn	Leu	Thr	Phe	Leu	Asp	Leu	Ser	Gln	Cys	Gln	Leu	Glu	Gln	Leu	Ser	
			500					505					510			
Pro	Thr	Ala	Phe	Asn	Ser	Leu	Ser	Ser	Leu	Gln	Val	Leu	Asn	Met	Ser	
		515					520					525				
His	Asn	Asn	Phe	Phe	Ser	Leu	Asp	Thr	Phe	Pro	Tyr	Lys	Cys	Leu	Asn	
	530					535					540					
Ser	Leu	Gln	Val	Leu	Asp	Tyr	Ser	Leu	Asn	His	Ile	Met	Thr	Ser	Lys	
545					550					555					560	
Lys	Gln	Glu	Leu	Gln	His	Phe	Pro	Ser	Ser	Leu	Ala	Phe	Leu	Asn	Leu	
				565					570					575		
Thr	Gln	Asn	Asp	Phe	Ala	Cys	Thr	Cys	Glu	His	Gln	Ser	Phe	Leu	Gln	
			580					585					590			
Trp	Ile	Lys	Asp	Gln	Arg	Gln	Leu	Leu	Val	Glu	Val	Glu	Arg	Met	Glu	
		595					600					605				
Cys	Ala	Thr	Pro	Ser	Asp	Lys	Gln	Gly	Met	Pro	Val	Leu	Ser	Leu	Asn	
	610					615					620					
Ile	Thr	Cys	Gln	Met	Asn	Lys	Thr	Ile	Ile	Gly	Val	Ser	Val	Leu	Ser	
625					630					635					640	
Val	Leu	Val	Val	Ser	Val	Val	Ala	Val	Leu	Val	Tyr	Lys	Phe	Tyr	Phe	
				645					650					655		
His	Leu	Met	Leu	Leu	Ala	Gly	Cys	Ile	Lys	Tyr	Gly	Arg	Gly	Glu	Asn	
			660					665					670			
Ile	Tyr	Asp	Ala	Phe	Val	Ile	Tyr	Ser	Ser	Gln	Asp	Glu	Asp	Trp	Val	
		675					680					685				
Arg	Asn	Glu	Leu	Val	Lys	Asn	Leu	Glu	Glu	Gly	Val	Pro	Pro	Phe	Gln	
	690					695					700					
Leu	Cys	Leu	His	Tyr	Arg	Asp	Phe	Ile	Pro	Gly	Val	Ala	Ile	Ala	Ala	
705					710					715					720	
Asn	Ile	Ile	His	Glu	Gly	Phe	His	Lys	Ser	Arg	Lys	Val	Ile	Val	Val	
				725					730					735		
Val	Ser	Gln	His	Phe	Ile	Gln	Ser	Arg	Trp	Cys	Ile	Phe	Glu	Tyr	Glu	
			740					745					750			
Ile	Ala	Gln	Thr	Trp	Gln	Phe	Leu	Ser	Ser	Arg	Ala	Gly	Ile	Ile	Phe	

755 760 765
 Ile Val Leu Gln Lys Val Glu Lys Thr Leu Leu Arg Gln Gln Val Glu
 770 775 780
 Leu Tyr Arg Leu Leu Ser Arg Asn Thr Tyr Leu Glu Trp Glu Asp Ser
 785 790 795 800
 Val Leu Gly Arg His Ile Phe Trp Arg Arg Leu Arg Lys Ala Leu Leu
 805 810 815
 Asp Gly Lys Ser Trp Asn Pro Glu Gly Thr Val Gly Thr Gly Cys Asn
 820 825 830
 Trp Gln Glu Ala Thr Ser Ile
 835

<210> 17
 <211> 782
 <212> PRT
 <213> Homo sapiens

<400> 17

Met Lys Pro Arg Ala Phe Arg Leu Arg Ser Leu Ser Pro Ser Pro Arg
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 Ile Gln Thr Ile Glu Asp Gly Ala Tyr Gln Ser Leu Ser His Leu Ser
 35 40 45
 Thr Leu Ile Leu Thr Gly Asn Pro Ile Gln Ser Leu Ala Leu Gly Ala
 50 55 60
 Phe Ser Gly Leu Ser Ser Leu Gln Lys Leu Val Ala Val Glu Thr Asn
 65 70 75 80
 Leu Ala Ser Leu Glu Asn Phe Pro Ile Gly His Leu Lys Thr Leu Lys
 85 90 95
 Glu Leu Asn Val Ala His Asn Leu Ile Gln Ser Phe Lys Leu Pro Glu
 100 105 110
 Tyr Phe Ser Asn Leu Thr Asn Leu Glu His Leu Asp Leu Ser Ser Asn
 115 120 125
 Lys Ile Gln Ser Ile Tyr Cys Thr Asp Leu Arg Val Leu His Gln Met
 130 135 140
 Pro Leu Leu Asn Leu Ser Leu Asp Leu Ser Leu Asn Pro Met Asn Phe
 145 150 155 160
 Ile Gln Pro Gly Ala Phe Lys Glu Ile Arg Leu His Lys Leu Thr Leu
 165 170 175
 Arg Asn Asn Phe Asp Ser Leu Asn Val Met Lys Thr Cys Ile Gln Gly
 180 185 190
 Leu Ala Gly Leu Glu Val His Arg Leu Val Leu Gly Glu Phe Arg Asn
 195 200 205

Glu Gly Asn Leu Glu Lys Phe Asp Lys Ser Ala Leu Glu Gly Leu Cys
 210 215 220
 Asn Leu Thr Ile Glu Glu Phe Arg Leu Ala Tyr Leu Asp Tyr Tyr Leu
 225 230 235 240
 Asp Asp Ile Ile Asp Leu Phe Asn Cys Leu Thr Asn Val Ser Ser Phe
 245 250 255
 Ser Leu Val Ser Val Thr Ile Glu Arg Val Lys Asp Phe Ser Tyr Asn
 260 265 270
 Phe Gly Trp Gln His Leu Glu Leu Val Asn Cys Lys Phe Gly Gln Phe
 275 280 285
 Pro Thr Leu Lys Leu Lys Ser Leu Lys Arg Leu Thr Phe Thr Ser Asn
 290 295 300
 Lys Gly Gly Asn Ala Phe Ser Glu Val Asp Leu Pro Ser Leu Glu Phe
 305 310 315 320
 Leu Asp Leu Ser Arg Asn Gly Leu Ser Phe Lys Gly Cys Cys Ser Gln
 325 330 335
 Ser Asp Phe Gly Thr Thr Ser Leu Lys Tyr Leu Asp Leu Ser Phe Asn
 340 345 350
 Gly Val Ile Thr Met Ser Ser Asn Phe Leu Gly Leu Glu Gln Leu Glu
 355 360 365
 His Leu Asp Phe Gln His Ser Asn Leu Lys Gln Met Ser Glu Phe Ser
 370 375 380
 Val Phe Leu Ser Leu Arg Asn Leu Ile Tyr Leu Asp Ile Ser His Thr
 385 390 395 400
 His Thr Arg Val Ala Phe Asn Gly Ile Phe Asn Gly Leu Ser Ser Leu
 405 410 415
 Glu Val Leu Lys Met Ala Gly Asn Ser Phe Gln Glu Asn Phe Leu Pro
 420 425 430
 Asp Ile Phe Thr Glu Leu Arg Asn Leu Thr Phe Leu Asp Leu Ser Gln
 435 440 445
 Cys Gln Leu Glu Gln Leu Ser Pro Thr Ala Phe Asn Ser Leu Ser Ser
 450 455 460
 Leu Gln Val Leu Asn Met Ser His Asn Asn Phe Phe Ser Leu Asp Thr
 465 470 475 480
 Phe Pro Tyr Lys Cys Leu Asn Ser Leu Gln Val Leu Asp Tyr Ser Leu
 485 490 495
 Asn His Ile Met Thr Ser Lys Lys Gln Glu Leu Gln His Phe Pro Ser
 500 505 510
 Ser Leu Ala Phe Leu Asn Leu Thr Gln Asn Asp Phe Ala Cys Thr Cys
 515 520 525
 Glu His Gln Ser Phe Leu Gln Trp Ile Lys Asp Gln Arg Gln Leu Leu

530 535 540
 Val Glu Val Glu Arg Met Glu Cys Ala Thr Pro Ser Asp Lys Gln Gly
 545 550 555 560
 Met Pro Val Leu Ser Leu Asn Ile Thr Cys Gln Met Asn Lys Thr Ile
 565 570 575
 Ile Gly Val Ser Val Leu Ser Val Leu Val Val Ser Val Val Ala Val
 580 585 590
 Leu Val Tyr Lys Phe Tyr Phe His Leu Met Leu Leu Ala Gly Cys Ile
 595 600 605
 Lys Tyr Gly Arg Gly Glu Asn Ile Tyr Asp Ala Phe Val Ile Tyr Ser
 610 615 620
 Ser Gln Asp Glu Asp Trp Val Arg Asn Glu Leu Val Lys Asn Leu Glu
 625 630 635 640
 Glu Gly Val Pro Pro Phe Gln Leu Cys Leu His Tyr Arg Asp Phe Ile
 645 650 655
 Pro Gly Val Ala Ile Ala Ala Asn Ile Ile His Glu Gly Phe His Lys
 660 665 670
 Ser Arg Lys Val Ile Val Val Val Ser Gln His Phe Ile Gln Ser Arg
 675 680 685
 Trp Cys Ile Phe Glu Tyr Glu Ile Ala Gln Thr Trp Gln Phe Leu Ser
 690 695 700
 Ser Arg Ala Gly Ile Ile Phe Ile Val Leu Gln Lys Val Glu Lys Thr
 705 710 715 720
 Leu Leu Arg Gln Gln Val Glu Leu Tyr Arg Leu Leu Ser Arg Asn Thr
 725 730 735
 Tyr Leu Glu Trp Glu Asp Ser Val Leu Gly Arg His Ile Phe Trp Arg
 740 745 750
 Arg Leu Arg Lys Ala Leu Leu Asp Gly Lys Ser Trp Asn Pro Glu Gly
 755 760 765
 Thr Val Gly Thr Gly Cys Asn Trp Gln Glu Ala Thr Ser Ile
 770 775 780

<210> 18
 <211> 799
 <212> PRT
 <213> Homo sapiens

<400> 18

Met Glu Leu Asn Phe Tyr Lys Ile Pro Asp Asn Leu Pro Phe Ser Thr
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 Lys Asn Leu Asp Leu Ser Phe Asn Pro Leu Arg His Leu Gly Ser Tyr
 20 25 30
 Ser Phe Phe Ser Phe Pro Glu Leu Gln Val Leu Asp Leu Ser Arg Cys
 35 40 45

Glu Ile Gln Thr Ile Glu Asp Gly Ala Tyr Gln Ser Leu Ser His Leu
 50 55 60
 Ser Thr Leu Ile Leu Thr Gly Asn Pro Ile Gln Ser Leu Ala Leu Gly
 65 70 75 80
 Ala Phe Ser Gly Leu Ser Ser Leu Gln Lys Leu Val Ala Val Glu Thr
 85 90 95
 Asn Leu Ala Ser Leu Glu Asn Phe Pro Ile Gly His Leu Lys Thr Leu
 100 105 110
 Lys Glu Leu Asn Val Ala His Asn Leu Ile Gln Ser Phe Lys Leu Pro
 115 120 125
 Glu Tyr Phe Ser Asn Leu Thr Asn Leu Glu His Leu Asp Leu Ser Ser
 130 135 140
 Asn Lys Ile Gln Ser Ile Tyr Cys Thr Asp Leu Arg Val Leu His Gln
 145 150 155 160
 Met Pro Leu Leu Asn Leu Ser Leu Asp Leu Ser Leu Asn Pro Met Asn
 165 170 175
 Phe Ile Gln Pro Gly Ala Phe Lys Glu Ile Arg Leu His Lys Leu Thr
 180 185 190
 Leu Arg Asn Asn Phe Asp Ser Leu Asn Val Met Lys Thr Cys Ile Gln
 195 200 205
 Gly Leu Ala Gly Leu Glu Val His Arg Leu Val Leu Gly Glu Phe Arg
 210 215 220
 Asn Glu Gly Asn Leu Glu Lys Phe Asp Lys Ser Ala Leu Glu Gly Leu
 225 230 235 240
 Cys Asn Leu Thr Ile Glu Glu Phe Arg Leu Ala Tyr Leu Asp Tyr Tyr
 245 250 255
 Leu Asp Asp Ile Ile Asp Leu Phe Asn Cys Leu Thr Asn Val Ser Ser
 260 265 270
 Phe Ser Leu Val Ser Val Thr Ile Glu Arg Val Lys Asp Phe Ser Tyr
 275 280 285
 Asn Phe Gly Trp Gln His Leu Glu Leu Val Asn Cys Lys Phe Gly Gln
 290 295 300
 Phe Pro Thr Leu Lys Leu Lys Ser Leu Lys Arg Leu Thr Phe Thr Ser
 305 310 315 320
 Asn Lys Gly Gly Asn Ala Phe Ser Glu Val Asp Leu Pro Ser Leu Glu
 325 330 335
 Phe Leu Asp Leu Ser Arg Asn Gly Leu Ser Phe Lys Gly Cys Cys Ser
 340 345 350
 Gln Ser Asp Phe Gly Thr Thr Ser Leu Lys Tyr Leu Asp Leu Ser Phe
 355 360 365
 Asn Gly Val Ile Thr Met Ser Ser Asn Phe Leu Gly Leu Glu Gln Leu

36/231

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<210> 19
<211> 639
<212> PRT
<213> Homo sapiens
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Leu	Arg	Asn 35	Asn	Phe	Asp	Ser	Leu 40	Asn	Val	Met	Lys	Thr 45	Cys	Ile	Gln
Gly	Leu 50	Ala	Gly	Leu	Glu	Val 55	His	Arg	Leu	Val 60	Leu	Gly	Glu	Phe	Arg
Asn 65	Glu	Gly	Asn	Leu 70	Glu	Lys	Phe	Asp	Lys 75	Ser	Ala	Leu	Glu	Gly	Leu 80
Cys	Asn	Leu	Thr 85	Ile	Glu	Glu	Phe	Arg 90	Leu	Ala	Tyr	Leu	Asp	Tyr 95	Tyr
Leu	Asp	Asp	Ile 100	Ile	Asp	Leu	Phe	Asn 105	Cys	Leu	Thr	Asn	Val 110	Ser	Ser
Phe	Ser	Leu 115	Val	Ser	Val	Thr	Ile 120	Glu	Arg	Val	Lys 125	Asp	Phe	Ser	Tyr
Asn 130	Phe	Gly	Trp	Gln	His	Leu 135	Glu	Leu	Val	Asn 140	Cys	Lys	Phe	Gly	Gln
Phe 145	Pro	Thr	Leu	Lys	Leu 150	Lys	Ser	Leu	Lys 155	Arg	Leu	Thr	Phe	Thr	Ser 160
Asn	Lys	Gly	Gly	Asn 165	Ala	Phe	Ser	Glu	Val 170	Asp	Leu	Pro	Ser	Leu	Glu
Phe	Leu	Asp	Leu 180	Ser	Arg	Asn	Gly	Leu 185	Ser	Phe	Lys	Gly	Cys 190	Cys	Ser
Gln	Ser	Asp 195	Phe	Gly	Thr	Thr	Ser 200	Leu	Lys	Tyr	Leu 205	Asp	Leu	Ser	Phe

Asn Gly Val Ile Thr Met Ser Ser Asn Phe Leu Gly Leu Glu Gln Leu
 210 215 220
 Glu His Leu Asp Phe Gln His Ser Asn Leu Lys Gln Met Ser Glu Phe
 225 230 235 240
 Ser Val Phe Leu Ser Leu Arg Asn Leu Ile Tyr Leu Asp Ile Ser His
 245 250 255
 Thr His Thr Arg Val Ala Phe Asn Gly Ile Phe Asn Gly Leu Ser Ser
 260 265 270
 Leu Glu Val Leu Lys Met Ala Gly Asn Ser Phe Gln Glu Asn Phe Leu
 275 280 285
 Pro Asp Ile Phe Thr Glu Leu Arg Asn Leu Thr Phe Leu Asp Leu Ser
 290 295 300
 Gln Cys Gln Leu Glu Gln Leu Ser Pro Thr Ala Phe Asn Ser Leu Ser
 305 310 315 320
 Ser Leu Gln Val Leu Asn Met Ser His Asn Asn Phe Phe Ser Leu Asp
 325 330 335
 Thr Phe Pro Tyr Lys Cys Leu Asn Ser Leu Gln Val Leu Asp Tyr Ser
 340 345 350
 Leu Asn His Ile Met Thr Ser Lys Lys Gln Glu Leu Gln His Phe Pro
 355 360 365
 Ser Ser Leu Ala Phe Leu Asn Leu Thr Gln Asn Asp Phe Ala Cys Thr
 370 375 380
 Cys Glu His Gln Ser Phe Leu Gln Trp Ile Lys Asp Gln Arg Gln Leu
 385 390 395 400
 Leu Val Glu Val Glu Arg Met Glu Cys Ala Thr Pro Ser Asp Lys Gln
 405 410 415
 Gly Met Pro Val Leu Ser Leu Asn Ile Thr Cys Gln Met Asn Lys Thr
 420 425 430
 Ile Ile Gly Val Ser Val Leu Ser Val Leu Val Val Ser Val Val Ala
 435 440 445
 Val Leu Val Tyr Lys Phe Tyr Phe His Leu Met Leu Leu Ala Gly Cys
 450 455 460
 Ile Lys Tyr Gly Arg Gly Glu Asn Ile Tyr Asp Ala Phe Val Ile Tyr
 465 470 475 480
 Ser Ser Gln Asp Glu Asp Trp Val Arg Asn Glu Leu Val Lys Asn Leu
 485 490 495
 Glu Glu Gly Val Pro Pro Phe Gln Leu Cys Leu His Tyr Arg Asp Phe
 500 505 510
 Ile Pro Gly Val Ala Ile Ala Ala Asn Ile Ile His Glu Gly Phe His
 515 520 525
 Lys Ser Arg Lys Val Ile Val Val Val Ser Gln His Phe Ile Gln Ser

530	535	540
Arg Trp Cys Ile Phe	Glu Tyr Glu Ile Ala	Gln Thr Trp Gln Phe Leu
545	550	555
Ser Ser Arg Ala Gly	Ile Ile Phe Ile Val	Leu Gln Lys Val Glu Lys
565	570	575
Thr Leu Leu Arg Gln	Gln Val Glu Leu Tyr Arg	Leu Leu Ser Arg Asn
580	585	590
Thr Tyr Leu Glu Trp	Glu Asp Ser Val Leu Gly	Arg His Ile Phe Trp
595	600	605
Arg Arg Leu Arg Lys	Ala Leu Leu Asp Gly Lys	Ser Trp Asn Pro Glu
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 <211> 3866
 <212> DNA
 <213> murine

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 aatattacct accaatgcat ggatcagaaa ctcagcaaag tccctgatga cattccttct 180
 tcaaccaaga acatagatct gagcttcaac cccttgaaga tottaaaaag ctatagcttc 240
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 cagagttttt cccaggaag tttctctgga ctaacaagtt tagagaatct ggtggctgtg 420
 gagacaaaat tggcctctct agaaagcttc cctattggac agcttataac cttaaagaaa 480
 ctcaatgtgg ctcaaatctt tacaattcc tgtaagttac ctgcatatct ttccaatctg 540
 acgaacctag tacatgtgga tctttcttat aactatattc aaactattac tgtcaacgac 600
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 attgacttca ttcaagacca agcctttcag ggaattaagc tccatgaact gactctaaga 720
 ggtaatttta atagctcaaa tataatgaaa acttgccttc aaaacctggc tggtttacac 780
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 gatttttcag atgatattgt taagttccat tgcttggcga atgtttctgc aatgtctctg 960
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 tcaatcatta gatgtcaact taagcagttt ccaactctgg atctaccctt tcttaaaagt 1080

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ttgggaacaa	acagcctgag	acacttagac	ctcagcttca	atgggtgccat	cattatgagt	1260
gccaatattca	tgggtctaga	agagctgcag	cacctggatt	ttcagcactc	tactttaaaa	1320
agggtcacag	aattctcagc	gttcttatcc	cttgaaaagc	tactttacct	tgacatctct	1380
tatactaaca	ccaaaattga	cttcgatggg	atattttcttg	gcttgaccag	tctcaacaca	1440
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			660					665					670			
Asp	Ala	Phe	Val	Ile	Tyr	Ser	Ser	Gln	Asn	Glu	Asp	Trp	Val	Arg	Asn	

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 Glu Leu Val Lys Asn Leu Glu Glu Gly Val Pro Arg Phe His Leu Cys
 690 695 700

 Leu His Tyr Arg Asp Phe Ile Pro Gly Val Ala Ile Ala Ala Asn Ile
 705 710 715 720

 Ile Gln Glu Gly Phe His Lys Ser Arg Lys Val Ile Val Val Val Ser
 725 730 735

 Arg His Phe Ile Gln Ser Arg Trp Cys Ile Phe Glu Tyr Glu Ile Ala
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 Gln Thr Trp Gln Phe Leu Ser Ser His Ser Gly Ile Ile Phe Ile Val
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 Leu Glu Lys Val Glu Lys Ser Leu Leu Arg Gln Gln Val Glu Leu Tyr
 770 775 780

 Arg Leu Leu Ser Arg Asn Thr Tyr Leu Glu Trp Glu Asp Asn Pro Leu
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 Gly Arg His Ile Phe Trp Arg Arg Leu Lys Asn Ala Leu Leu Asp Gly
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 taagaacata ctagaagtcc cttctgctag gacaacgagg atcatgggag accacctgga 720

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 <213> Homo sapiens

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 35 40 45
 Glu Arg Leu Leu Leu Ser Phe Asn Tyr Ile Arg Thr Val Thr Ala Ser
 50 55 60
 Ser Phe Pro Phe Leu Glu Gln Leu Gln Leu Leu Glu Leu Gly Ser Gln
 65 70 75 80
 Tyr Thr Pro Leu Thr Ile Asp Lys Glu Ala Phe Arg Asn Leu Pro Asn
 85 90 95
 Leu Arg Ile Leu Asp Leu Gly Ser Ser Lys Ile Tyr Phe Leu His Pro
 100 105 110
 Asp Ala Phe Gln Gly Leu Phe His Leu Phe Glu Leu Arg Leu Tyr Phe
 115 120 125
 Cys Gly Leu Ser Asp Ala Val Leu Lys Asp Gly Tyr Phe Arg Asn Leu

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Lys Ala Leu Thr Arg	Leu Asp Leu Ser Lys	Asn Gln Ile Arg Ser Leu
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Tyr Leu His Pro	Phe Gly Lys Leu Asn Ser	Leu Lys Ser Ile Asp
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Phe Ser Ser Asn Gln Ile	Phe Leu Val Cys Glu His	Glu Leu Glu Pro
	180	190
Leu Gln Gly Lys Thr	Leu Ser Phe Phe Ser	Leu Ala Ala Asn Ser Leu
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Tyr Ser Arg Val Ser	Val Asp Trp Gly Lys Cys	Met Asn Pro Phe Arg
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Asn Met Val Leu Glu	Ile Leu Asp Val Ser	Gly Asn Gly Trp Thr Val
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Asp Ile Thr Gly Asn	Phe Ser Asn Ala Ile	Ser Lys Ser Gln Ala Phe
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Ser Leu Ile Leu Ala	His His Ile Met Gly	Ala Gly Phe Gly Phe His
	260	265
Asn Ile Lys Asp Pro	Asp Gln Asn Thr Phe	Ala Gly Leu Ala Arg Ser
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Ser Val Arg His Leu	Asp Leu Ser His Gly	Phe Val Phe Ser Leu Asn
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Ser Arg Val Phe Glu	Thr Leu Lys Asp Leu	Lys Val Leu Asn Leu Ala
	305	310
Tyr Asn Lys Ile Asn	Lys Ile Ala Asp Glu	Ala Phe Tyr Gly Leu Asp
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Asn Leu Gln Val Leu	Asn Leu Ser Tyr Asn	Leu Leu Gly Glu Leu Tyr
	340	345
Ser Ser Asn Phe Tyr	Gly Leu Pro Lys Val	Ala Tyr Ile Asp Leu Gln
	355	360
Lys Asn His Ile Ala	Ile Ile Gln Asp Gln	Thr Phe Lys Phe Leu Glu
	370	375
Lys Leu Gln Thr Leu	Asp Leu Arg Asp Asn	Ala Leu Thr Thr Ile His
	385	390
Phe Ile Pro Ser Ile	Pro Asp Ile Phe Leu	Ser Gly Asn Lys Leu Val
	405	410
Thr Leu Pro Lys Ile	Asn Leu Thr Ala Asn	Leu Ile His Leu Ser Glu
	420	425
Asn Arg Leu Glu Asn	Leu Asp Ile Leu Tyr	Phe Leu Leu Arg Val Pro
	435	440
His Leu Gln Ile Leu	Ile Leu Asn Gln Asn	Arg Phe Ser Ser Cys Ser
	450	455
Gly Asp Gln Thr Pro	Ser Glu Asn Pro Ser	Leu Glu Gln Leu Phe Leu

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Gly Glu Asn Met	Leu Gln Leu Ala Trp	Glu Thr Glu Leu Cys Trp	Asp			
	485	490	495			
Val Phe Glu Gly	Leu Ser His Leu Gln Val Leu Tyr Leu	Asn His Asn				
	500	505	510			
Tyr Leu Asn Ser	Leu Pro Pro Gly Val Phe Ser His Leu Thr Ala Leu					
	515	520	525			
Arg Gly Leu Ser	Leu Asn Ser Asn Arg Leu Thr Val Leu Ser His Asn					
	530	535	540			
Asp Leu Pro Ala	Asn Leu Glu Ile Leu Asp Ile Ser Arg Asn Gln Leu					
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Leu Ala Pro Asn	Pro Asp Val Phe Val Ser Leu Ser Val Leu Asp Ile					
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Thr His Asn Lys	Phe Ile Cys Glu Cys Glu Leu Ser Thr Phe Ile Asn					
	580	585	590			
Trp Leu Asn His	Thr Asn Val Thr Ile Ala Gly Pro Pro Ala Asp Ile					
	595	600	605			
Tyr Cys Val Tyr	Pro Asp Ser Phe Ser Gly Val Ser Leu Phe Ser Leu					
	610	615	620			
Ser Thr Glu Gly	Cys Asp Glu Glu Glu Val Leu Lys Ser Leu Lys Phe					
	625	630	635			640
Ser Leu Phe Ile	Val Cys Thr Val Thr Leu Thr Leu Phe Leu Met Thr					
	645	650	655			
Ile Leu Thr Val	Thr Lys Phe Arg Gly Phe Cys Phe Ile Cys Tyr Lys					
	660	665	670			
Thr Ala Gln Arg	Leu Val Phe Lys Asp His Pro Gln Gly Thr Glu Pro					
	675	680	685			
Asp Met Tyr Lys	Tyr Asp Ala Tyr Leu Cys Phe Ser Ser Lys Asp Phe					
	690	695	700			
Thr Trp Val Gln	Asn Ala Leu Leu Lys His Leu Asp Thr Gln Tyr Ser					
	705	710	715			720
Asp Gln Asn Arg	Phe Asn Leu Cys Phe Glu Glu Arg Asp Phe Val Pro					
	725	730	735			
Gly Glu Asn Arg	Ile Ala Asn Ile Gln Asp Ala Ile Trp Asn Ser Arg					
	740	745	750			
Lys Ile Val Cys	Leu Val Ser Arg His Phe Leu Arg Asp Gly Trp Cys					
	755	760	765			
Leu Glu Ala Phe	Ser Tyr Ala Gln Gly Arg Cys Leu Ser Asp Leu Asn					
	770	775	780			
Ser Ala Leu Ile	Met Val Val Val Gly Ser Leu Ser Gln Tyr Gln Leu					
	785	790	795			800
Met Lys His Gln	Ser Ile Arg Gly Phe Val Gln Lys Gln Gln Tyr Leu					

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 Arg Trp Pro Glu Asp Leu Gln Asp Val Gly Trp Phe Leu His Lys Leu
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 Ile Pro Leu Gln Thr Val Ala Thr Ile Ser
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 35 40 45
 Glu Arg Leu Leu Leu Ser Phe Asn Tyr Ile Arg Thr Val Thr Ala Ser
 50 55 60
 Ser Phe Pro Phe Leu Glu Gln Leu Gln Leu Leu Glu Leu Gly Ser Gln
 65 70 75 80
 Tyr Thr Pro Leu Thr Ile Asp Lys Glu Ala Phe Arg Asn Leu Pro Asn
 85 90 95
 Leu Arg Ile Leu Asp Leu Gly Ser Ser Lys Ile Tyr Phe Leu His Pro
 100 105 110
 Asp Ala Phe Gln Gly Leu Phe His Leu Phe Glu Leu Arg Leu Tyr Phe
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 Cys Gly Leu Ser Asp Ala Val Leu Lys Asp Gly Tyr Phe Arg Asn Leu
 130 135 140
 Lys Ala Leu Thr Arg Leu Asp Leu Ser Lys Asn Gln Ile Arg Ser Leu
 145 150 155 160
 Tyr Leu His Pro Ser Phe Gly Lys Leu Asn Ser Leu Lys Ser Ile Asp
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 Phe Ser Ser Asn Gln Ile Phe Leu Val Cys Glu His Glu Leu Glu Pro
 180 185 190
 Leu Gln Gly Lys Thr Leu Ser Phe Phe Ser Leu Ala Ala Asn Ser Leu
 195 200 205
 Tyr Ser Arg Val Ser Val Asp Trp Gly Lys Cys Met Asn Pro Phe Arg
 210 215 220
 Asn Met Val Leu Glu Ile Val Asp Val Ser Gly Asn Gly Trp Thr Val
 225 230 235 240

Asp Ile Thr Gly Asn Phe Ser Asn Ala Ile Ser Lys Ser Gln Ala Phe
 245 250 255
 Ser Leu Ile Leu Ala His His Ile Met Gly Ala Gly Phe Gly Phe His
 260 265 270
 Asn Ile Lys Asp Pro Asp Gln Asn Thr Phe Ala Gly Leu Ala Arg Ser
 275 280 285
 Ser Val Arg His Leu Asp Leu Ser His Gly Phe Val Phe Ser Leu Asn
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 Ser Arg Val Phe Glu Thr Leu Lys Asp Leu Lys Val Leu Asn Leu Ala
 305 310 315 320
 Tyr Asn Lys Ile Asn Lys Ile Ala Asp Glu Ala Phe Tyr Gly Leu Asp
 325 330 335
 Asn Leu Gln Val Leu Asn Leu Ser Tyr Asn Leu Leu Gly Glu Leu Cys
 340 345 350
 Ser Ser Asn Phe Tyr Gly Leu Pro Lys Val Ala Tyr Ile Asp Leu Gln
 355 360 365
 Lys Asn His Ile Ala Ile Ile Gln Asp Gln Thr Phe Lys Phe Leu Glu
 370 375 380
 Lys Leu Gln Thr Leu Asp Leu Arg Asp Asn Ala Leu Thr Thr Ile His
 385 390 395 400
 Phe Ile Pro Ser Ile Pro Asp Ile Phe Leu Ser Gly Asn Lys Leu Val
 405 410 415
 Thr Leu Pro Lys Ile Asn Leu Thr Ala Asn Leu Ile His Leu Ser Glu
 420 425 430
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 Tyr Leu Asn Ser Leu Pro Pro Gly Val Phe Ser His Leu Thr Ala Leu
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 Arg Gly Leu Ser Leu Asn Ser Asn Arg Leu Thr Val Leu Ser His Asn
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 35 40 45
 Ser His Asn Asp Leu Pro Ala Asn Leu Glu Ile Leu Asp Ile Ser Arg
 50 55 60
 Asn Gln Leu Leu Ala Pro Asn Pro Asp Val Phe Val Ser Leu Ser Val
 65 70 75 80
 Leu Asp Ile Thr His Asn Lys Phe Ile Cys Glu Cys Glu Leu Ser Thr
 85 90 95
 Phe Ile Asn Trp Leu Asn His Thr Asn Val Thr Ile Ala Gly Pro Pro
 100 105 110
 Ala Asp Ile Tyr Cys Val Tyr Pro Asp Ser Phe Ser Gly Val Ser Leu
 115 120 125
 Phe Ser Leu Ser Thr Glu Gly Cys Asp Glu Glu Glu Val Leu Lys Ser
 130 135 140
 Leu Lys Phe Ser Leu Phe Ile Val Cys Thr Val Thr Leu Thr Leu Phe
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 Cys Tyr Lys Thr Ala Gln Arg Leu Val Phe Lys Asp His Pro Gln Gly
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<212> DNA

<213> Homo sapiens

<400> 33

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 cacataccag acatctcccc agcgtccttt cacagactgg accatctggg agagatcgat 420
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<211> 1049

<212> PRT

<213> Homo sapiens

<400> 34

Met Val Phe Pro Met Trp Thr Leu Lys Arg Gln Ile Leu Ile Leu Phe
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20 25 30

Thr Leu Pro Cys Asp Val Thr Leu Asp Val Pro Lys Asn His Val Ile
35 40 45

Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro Gly Gly Ile Pro
50 55 60

Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn His Ile Pro Asp Ile
65 70 75 80

Ser Pro Ala Ser Phe His Arg Leu Asp His Leu Val Glu Ile Asp Phe
85 90 95

Arg Cys Asn Cys Val Pro Ile Pro Leu Gly Ser Lys Asn Asn Met Cys
100 105 110

Ile Lys Arg Leu Gln Ile Lys Pro Arg Ser Phe Ser Gly Leu Thr Tyr
115 120 125

Leu Lys Ser Leu Tyr Leu Asp Gly Asn Gln Leu Leu Glu Ile Pro Gln
130 135 140

Gly Leu Pro Pro Ser Leu Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile
145 150 155 160

Phe Ser Ile Arg Lys Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile
165 170 175

Leu Tyr Leu Gly Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser
180 185 190

Tyr Ser Ile Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val
195 200 205

Leu Ser Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro
210 215 220

Ser Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile
225 230 235 240

Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp Leu
245 250 255

Ser Gly Asn Cys Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys Ala Pro

Cys	Lys	Asn	Asn	Ser	Pro	Leu	Gln	Ile	Pro	Val	Asn	Ala	Phe	Asp	Ala	
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Leu	Thr	Glu	Leu	Lys	Val	Leu	Arg	Leu	His	Ser	Asn	Ser	Leu	Gln	His	
	290					295					300					
Val	Pro	Pro	Arg	Trp	Phe	Lys	Asn	Ile	Asn	Lys	Leu	Gln	Glu	Leu	Asp	
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Leu	Ser	Gln	Asn	Phe	Leu	Ala	Lys	Glu	Ile	Gly	Asp	Ala	Lys	Phe	Leu	
				325					330					335		
His	Phe	Leu	Pro	Ser	Leu	Ile	Gln	Leu	Asp	Leu	Ser	Phe	Asn	Phe	Glu	
			340					345					350			
Leu	Gln	Val	Tyr	Arg	Ala	Ser	Met	Asn	Leu	Ser	Gln	Ala	Phe	Ser	Ser	
		355					360					365				
Leu	Lys	Ser	Leu	Lys	Ile	Leu	Arg	Ile	Arg	Gly	Tyr	Val	Phe	Lys	Glu	
	370					375					380					
Leu	Lys	Ser	Phe	Asn	Leu	Ser	Pro	Leu	His	Asn	Leu	Gln	Asn	Leu	Glu	
385					390					395					400	
Val	Leu	Asp	Leu	Gly	Thr	Asn	Phe	Ile	Lys	Ile	Ala	Asn	Leu	Ser	Met	
				405					410					415		
Phe	Lys	Gln	Phe	Lys	Arg	Leu	Lys	Val	Ile	Asp	Leu	Ser	Val	Asn	Lys	
			420					425					430			
Ile	Ser	Pro	Ser	Gly	Asp	Ser	Ser	Glu	Val	Gly	Phe	Cys	Ser	Asn	Ala	
		435					440					445				
Arg	Thr	Ser	Val	Glu	Ser	Tyr	Glu	Pro	Gln	Val	Leu	Glu	Gln	Leu	His	
	450					455					460					
Tyr	Phe	Arg	Tyr	Asp	Lys	Tyr	Ala	Arg	Ser	Cys	Arg	Phe	Lys	Asn	Lys	
465					470					475					480	
Glu	Ala	Ser	Phe	Met	Ser	Val	Asn	Glu	Ser	Cys	Tyr	Lys	Tyr	Gly	Gln	
				485					490					495		
Thr	Leu	Asp	Leu	Ser	Lys	Asn	Ser	Ile	Phe	Phe	Val	Lys	Ser	Ser	Asp	
			500					505					510			
Phe	Gln	His	Leu	Ser	Phe	Leu	Lys	Cys	Leu	Asn	Leu	Ser	Gly	Asn	Leu	
		515					520					525				
Ile	Ser	Gln	Thr	Leu	Asn	Gly	Ser	Glu	Phe	Gln	Pro	Leu	Ala	Glu	Leu	
	530					535					540					
Arg	Tyr	Leu	Asp	Phe	Ser	Asn	Asn	Arg	Leu	Asp	Leu	Leu	His	Ser	Thr	
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Ala	Phe	Glu	Glu	Leu	His	Lys	Leu	Glu	Val	Leu	Asp	Ile	Ser	Ser	Asn	
				565					570					575		
Ser	His	Tyr	Phe	Gln	Ser	Glu	Gly	Ile	Thr	His	Met	Leu	Asn	Phe	Thr	
			580					585					590			
Lys	Asn	Leu	Lys	Val	Leu	Gln	Lys	Leu	Met	Met	Asn	Asp	Asn	Asp	Ile	

595				600				605							
Ser	Ser	Ser	Thr	Ser	Arg	Thr	Met	Glu	Ser	Glu	Ser	Leu	Arg	Thr	Leu
610				615				620							
Glu	Phe	Arg	Gly	Asn	His	Leu	Asp	Val	Leu	Trp	Arg	Glu	Gly	Asp	Asn
625				630				635				640			
Arg	Tyr	Leu	Gln	Leu	Phe	Lys	Asn	Leu	Leu	Lys	Leu	Glu	Glu	Leu	Asp
645				650				655							
Ile	Ser	Lys	Asn	Ser	Leu	Ser	Phe	Leu	Pro	Ser	Gly	Val	Phe	Asp	Gly
660				665				670							
Met	Pro	Pro	Asn	Leu	Lys	Asn	Leu	Ser	Leu	Ala	Lys	Asn	Gly	Leu	Lys
675				680				685							
Ser	Phe	Ser	Trp	Lys	Lys	Leu	Gln	Cys	Leu	Lys	Asn	Leu	Glu	Thr	Leu
690				695				700							
Asp	Leu	Ser	His	Asn	Gln	Leu	Thr	Thr	Val	Pro	Glu	Arg	Leu	Ser	Asn
705				710				715				720			
Cys	Ser	Arg	Ser	Leu	Lys	Asn	Leu	Ile	Leu	Lys	Asn	Asn	Gln	Ile	Arg
725				730				735							
Ser	Leu	Thr	Lys	Tyr	Phe	Leu	Gln	Asp	Ala	Phe	Gln	Leu	Arg	Tyr	Leu
740				745				750							
Asp	Leu	Ser	Ser	Asn	Lys	Ile	Gln	Met	Ile	Gln	Lys	Thr	Ser	Phe	Pro
755				760				765							
Glu	Asn	Val	Leu	Asn	Asn	Leu	Lys	Met	Leu	Leu	Leu	His	His	Asn	Arg
770				775				780							
Phe	Leu	Cys	Thr	Cys	Asp	Ala	Val	Trp	Phe	Val	Trp	Trp	Val	Asn	His
785				790				795				800			
Thr	Glu	Val	Thr	Ile	Pro	Tyr	Leu	Ala	Thr	Asp	Val	Thr	Cys	Val	Gly
805				810				815							
Pro	Gly	Ala	His	Lys	Gly	Gln	Ser	Val	Ile	Ser	Leu	Asp	Leu	Tyr	Thr
820				825				830							
Cys	Glu	Leu	Asp	Leu	Thr	Asn	Leu	Ile	Leu	Phe	Ser	Leu	Ser	Ile	Ser
835				840				845							
Val	Ser	Leu	Phe	Leu	Met	Val	Met	Met	Thr	Ala	Ser	His	Leu	Tyr	Phe
850				855				860							
Trp	Asp	Val	Trp	Tyr	Ile	Tyr	His	Phe	Cys	Lys	Ala	Lys	Ile	Lys	Gly
865				870				875				880			
Tyr	Gln	Arg	Leu	Ile	Ser	Pro	Asp	Cys	Cys	Tyr	Asp	Ala	Phe	Ile	Val
885				890				895							
Tyr	Asp	Thr	Lys	Asp	Pro	Ala	Val	Thr	Glu	Trp	Val	Leu	Ala	Glu	Leu
900				905				910							
Val	Ala	Lys	Leu	Glu	Asp	Pro	Arg	Glu	Lys	His	Phe	Asn	Leu	Cys	Leu
915				920				925							
Glu	Glu	Arg	Asp	Trp	Leu	Pro	Gly	Gln	Pro	Val	Leu	Glu	Asn	Leu	Ser

930 935 940
 Gln Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys
 945 950 955 960
 Tyr Ala Lys Thr Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His Gln
 965 970 975
 Arg Leu Met Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe Leu Glu
 980 985 990
 Lys Pro Phe Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg Leu Cys
 995 1000 1005
 Gly Ser Ser Val Leu Glu Trp Pro Thr Asn Pro Gln Ala His Pro
 1010 1015 1020
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 Val Ala Tyr Ser Gln Val Phe Lys Glu Thr Val
 1040 1045

<210> 35
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 <212> PRT
 <213> Homo sapiens

<400> 35

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 Asn Ile Ile Leu Ile Ser Lys Leu Leu Gly Ala Arg Trp Phe Pro Lys
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 Thr Leu Pro Cys Asp Val Thr Leu Asp Val Pro Lys Asn His Val Ile
 35 40 45
 Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro Gly Gly Ile Pro
 50 55 60
 Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn His Ile Pro Asp Ile
 65 70 75 80
 Ser Pro Ala Ser Phe His Arg Leu Asp His Leu Val Glu Ile Asp Phe
 85 90 95
 Arg Cys Asn Cys Val Pro Ile Pro Leu Gly Ser Lys Asn Asn Met Cys
 100 105 110
 Ile Lys Arg Leu Gln Ile Lys Pro Arg Ser Phe Ser Gly Leu Thr Tyr
 115 120 125
 Leu Lys Ser Leu Tyr Leu Asp Gly Asn Gln Leu Leu Glu Ile Pro Gln
 130 135 140
 Gly Leu Pro Pro Ser Leu Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile
 145 150 155 160
 Phe Ser Ile Arg Lys Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile
 165 170 175

Leu Tyr Leu Gly Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser
 180 185 190
 Tyr Ser Ile Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val
 195 200 205
 Leu Ser Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro
 210 215 220
 Ser Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile
 225 230 235 240
 Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp Leu
 245 250 255
 Ser Gly Asn Cys Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys Ala Pro
 260 265 270
 Cys Lys Asn Asn Ser Pro Leu Gln Ile Pro Val Asn Ala Phe Asp Ala
 275 280 285
 Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn Ser Leu Gln His
 290 295 300
 Val Pro Pro Arg Trp Phe Lys Asn Ile Asn Lys Leu Gln Glu Leu Asp
 305 310 315 320
 Leu Ser Gln Asn Phe Leu Ala Lys Glu Ile Gly Asp Ala Lys Phe Leu
 325 330 335
 His Phe Leu Pro Ser Leu Ile Gln Leu Asp Leu Ser Phe Asn Phe Glu
 340 345 350
 Leu Gln Val Tyr Arg Ala Ser Met Asn Leu Ser Gln Ala Phe Ser Ser
 355 360 365
 Leu Lys Ser Leu Lys Ile Leu Arg Ile Arg Gly Tyr Val Phe Lys Glu
 370 375 380
 Leu Lys Ser Phe Asn Leu Ser Pro Leu His Asn Leu Gln Asn Leu Glu
 385 390 395 400
 Val Leu Asp Leu Gly Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met
 405 410 415
 Phe Lys Gln Phe Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys
 420 425 430
 Ile Ser Pro Ser Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala
 435 440 445
 Arg Thr Ser Val Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His
 450 455 460
 Tyr Phe Arg Tyr Asp Lys Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys
 465 470 475 480
 Glu Ala Ser Phe Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly Gln
 485 490 495
 Thr Leu Asp Leu Ser Lys Asn Ser Ile Phe Phe Val Lys Ser Ser Asp

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Phe	Gln	His	Leu	Ser	Phe	Leu	Lys	Cys	Leu	Asn	Leu	Ser	Gly	Asn	Leu		
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Ile	Ser	Gln	Thr	Leu	Asn	Gly	Ser	Glu	Phe	Gln	Pro	Leu	Ala	Glu	Leu		
		530				535					540						
Arg	Tyr	Leu	Asp	Phe	Ser	Asn	Asn	Arg	Leu	Asp	Leu	Leu	His	Ser	Thr		
545					550					555					560		
Ala	Phe	Glu	Glu	Leu	His	Lys	Leu	Glu	Val	Leu	Asp	Ile	Ser	Ser	Asn		
				565					570						575		
Ser	His	Tyr	Phe	Gln	Ser	Glu	Gly	Ile	Thr	His	Met	Leu	Asn	Phe	Thr		
			580					585					590				
Lys	Asn	Leu	Lys	Val	Leu	Gln	Lys	Leu	Met	Met	Asn	Asp	Asn	Asp	Ile		
		595					600					605					
Ser	Ser	Ser	Thr	Ser	Arg	Thr	Met	Glu	Ser	Glu	Ser	Leu	Arg	Thr	Leu		
		610				615					620						
Glu	Phe	Arg	Gly	Asn	His	Leu	Asp	Val	Leu	Trp	Arg	Glu	Gly	Asp	Asn		
625				630						635					640		
Arg	Tyr	Leu	Gln	Leu	Phe	Lys	Asn	Leu	Leu	Lys	Leu	Glu	Glu	Leu	Asp		
				645					650						655		
Ile	Ser	Lys	Asn	Ser	Leu	Ser	Phe	Leu	Pro	Ser	Gly	Val	Phe	Asp	Gly		
			660					665					670				
Met	Pro	Pro	Asn	Leu	Lys	Asn	Leu	Ser	Leu	Ala	Lys	Asn	Gly	Leu	Lys		
		675					680					685					
Ser	Phe	Ser	Trp	Lys	Lys	Leu	Gln	Cys	Leu	Lys	Asn	Leu	Glu	Thr	Leu		
		690				695					700						
Asp	Leu	Ser	His	Asn	Gln	Leu	Thr	Thr	Val	Pro	Glu	Arg	Leu	Ser	Asn		
705				710						715					720		
Cys	Ser	Arg	Ser	His	Lys	Asn	Leu	Ile	Leu	Lys	Asn	Asn	Gln	Ile	Arg		
				725				730						735			
Ser	Pro	Thr	Lys	Tyr	Phe	Leu	Gln	Asp	Ala	Phe	Gln	Leu	Arg	Tyr	Leu		
			740					745					750				
Asp	Leu	Ser	Ser	Asn	Lys	Ile	Gln	Met	Ile	Gln	Lys	Thr	Ser	Phe	Pro		
		755					760					765					
Glu	Asn	Val	Leu	Asn	Asn	Leu	Lys	Met	Leu	Leu	Leu	His	His	Asn	Arg		
		770				775						780					
Phe	Leu	Cys	Thr	Cys	Asp	Ala	Val	Trp	Phe	Val	Trp	Trp	Val	Asn	His		
785					790					795					800		
Thr	Glu	Val	Thr	Ile	Pro	Tyr	Leu	Ala	Thr	Asp	Val	Thr	Cys	Val	Gly		
				805					810					815			
Pro	Gly	Ala	His	Lys	Gly	Gln	Ser	Val	Ile	Ser	Leu	Asp	Leu	Tyr	Thr		
			820					825					830				
Cys	Glu	Leu	Asp	Leu	Thr	Asn	Leu	Ile	Leu	Phe	Ser	Leu	Ser	Ile	Ser		

835	840	845
Val Ser Leu Phe Leu Met	Val Met Met Thr Ala	Ser His Leu Tyr Phe
850	855	860
Trp Asp Val Trp Tyr Ile	Tyr His Phe Cys Lys	Ala Lys Ile Lys Gly
865	870	875 880
Tyr Gln Arg Leu Ile Ser	Pro Asp Cys Cys Tyr	Asp Ala Phe Ile Val
885	890	895
Tyr Asp Thr Lys Asp Pro	Ala Val Thr Glu Trp	Val Leu Ala Glu Leu
900	905	910
Val Ala Lys Leu Glu Asp	Pro Arg Glu Lys His	Phe Asn Leu Cys Leu
915	920	925
Glu Glu Arg Asp Trp Leu	Pro Gly Gln Pro Val	Leu Glu Asn Leu Ser
930	935	940
Gln Ser Ile Gln Leu Ser	Lys Lys Thr Val Phe	Val Met Thr Asp Lys
945	950	955 960
Tyr Ala Lys Thr Glu Asn	Phe Lys Ile Ala Phe	Tyr Leu Ser His Gln
965	970	975
Arg Leu Met Asp Glu Lys	Val Asp Val Ile Ile	Leu Ile Phe Leu Glu
980	985	990
Lys Pro Phe Gln Lys Ser	Lys Phe Leu Gln Leu	Arg Lys Arg Leu Cys
995	1000	1005
Gly Ser Ser Val Leu Glu	Trp Pro Thr Asn Pro	Gln Ala His Pro
1010	1015	1020
Tyr Phe Trp Gln Cys Leu	Lys Asn Ala Leu Ala	Thr Asp Asn His
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Val Ala Tyr Ser Gln Val	Phe Lys Glu Thr Val	
1040	1045	

<210> 36
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<400> 36

Met Val Phe Pro Met Trp	Thr Leu Lys Arg Gln	Ile Leu Ile Leu Phe
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Asn Ile Ile Leu Ile Ser	Lys Leu Leu Gly Ala	Arg Trp Phe Pro Lys
20	25	30
Thr Leu Pro Cys Asp Val	Thr Leu Asp Val Pro	Lys Asn His Val Ile
35	40	45
Val Asp Cys Thr Asp Lys	His Leu Thr Glu Ile	Pro Gly Gly Ile Pro
50	55	60
Thr Asn Thr Thr Asn Leu	Thr Leu Thr Ile Asn	His Ile Pro Asp Ile
65	70	75 80

Ser Pro Ala Ser Phe His Arg Leu Asp His Leu Val Glu Ile Asp Phe
 85 90 95
 Arg Cys Asn Cys Val Pro Ile Pro Leu Gly Ser Lys Asn Asn Met Cys
 100 105 110
 Ile Lys Arg Leu Gln Ile Lys Pro Arg Ser Phe Ser Gly Leu Thr Tyr
 115 120 125
 Leu Lys Ser Leu Tyr Leu Asp Gly Asn Gln Leu Leu Glu Ile Pro Gln
 130 135 140
 Gly Leu Pro Pro Ser Leu Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile
 145 150 155 160
 Phe Ser Ile Arg Lys Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile
 165 170 175
 Leu Tyr Leu Gly Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser
 180 185 190
 Tyr Ser Ile Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val
 195 200 205
 Leu Ser Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro
 210 215 220
 Ser Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile
 225 230 235 240
 Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp Leu
 245 250 255
 Ser Gly Asn Cys Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys Ala Pro
 260 265 270
 Cys Lys Asn Asn Ser Pro Leu Gln Ile Pro Val Asn Ala Phe Asp Ala
 275 280 285
 Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn Ser Leu Gln His
 290 295 300
 Val Pro Pro Arg Trp Phe Lys Asn Ile Asn Lys Leu Gln Glu Leu Asp
 305 310 315 320
 Leu Ser Gln Asn Phe Leu Ala Lys Glu Ile Gly Asp Ala Lys Phe Leu
 325 330 335
 His Phe Leu Pro Ser Leu Ile Gln Leu Asp Leu Ser Phe Asn Phe Glu
 340 345 350
 Leu Gln Val Tyr Arg Ala Ser Met Asn Leu Ser Gln Ala Phe Ser Ser
 355 360 365
 Leu Lys Ser Leu Lys Ile Leu Arg Ile Arg Gly Tyr Val Phe Lys Glu
 370 375 380
 Leu Lys Ser Phe Asn Leu Ser Pro Leu His Asn Leu Gln Asn Leu Glu
 385 390 395 400
 Val Leu Asp Leu Gly Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met

Phe	Lys	Gln	Phe	Lys	Arg	Leu	Lys	Val	Ile	Asp	Leu	Ser	Val	Asn	Lys
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Ile	Ser	Pro	Ser	Gly	Asp	Ser	Ser	Glu	Val	Gly	Phe	Cys	Ser	Asn	Ala
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Arg	Thr	Ser	Val	Glu	Ser	Tyr	Glu	Pro	Gln	Val	Leu	Glu	Gln	Leu	His
	450					455					460				
Tyr	Phe	Arg	Tyr	Asp	Lys	Tyr	Ala	Arg	Ser	Cys	Arg	Phe	Lys	Asn	Lys
465					470					475					480
Glu	Ala	Ser	Phe	Met	Ser	Val	Asn	Glu	Ser	Cys	Tyr	Lys	Tyr	Gly	Gln
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Thr	Leu	Asp	Leu	Ser	Lys	Asn	Ser	Ile	Phe	Phe	Val	Lys	Ser	Ser	Asp
			500					505					510		
Phe	Gln	His	Leu	Ser	Phe	Leu	Lys	Cys	Leu	Asn	Leu	Ser	Gly	Asn	Leu
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Ile	Ser	Gln	Thr	Leu	Asn	Gly	Ser	Glu	Phe	Gln	Pro	Leu	Ala	Glu	Leu
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Arg	Tyr	Leu	Asp	Phe	Ser	Asn	Asn	Arg	Leu	Asp	Leu	Leu	His	Ser	Thr
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Ala	Phe	Glu	Glu	Leu	His	Lys	Leu	Glu	Val	Leu	Asp	Ile	Ser	Ser	Asn
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Ser	His	Tyr	Phe	Gln	Ser	Glu	Gly	Ile	Thr	His	Met	Leu	Asn	Phe	Thr
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Lys	Asn	Leu	Lys	Val	Leu	Gln	Lys	Leu	Met	Met	Asn	Asp	Asn	Asp	Ile
	595						600					605			
Ser	Ser	Ser	Thr	Ser	Arg	Thr	Met	Glu	Ser	Glu	Ser	Leu	Arg	Thr	Leu
	610					615					620				
Glu	Phe	Arg	Gly	Asn	His	Leu	Asp	Val	Leu	Trp	Arg	Glu	Gly	Asp	Asn
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Arg	Tyr	Leu	Gln	Leu	Phe	Lys	Asn	Leu	Leu	Lys	Leu	Glu	Glu	Leu	Asp
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Ile	Ser	Lys	Asn	Ser	Leu	Ser	Phe	Leu	Pro	Ser	Gly	Val	Phe	Asp	Gly
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		675					680					685			
Ser	Phe	Ser	Trp	Lys	Lys	Leu	Gln	Cys	Leu	Lys	Asn	Leu	Glu	Thr	Leu
	690					695					700				
Asp	Leu	Ser	His	Asn	Gln	Leu	Thr	Thr	Val	Pro	Glu	Arg	Leu	Ser	Asn
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Cys	Ser	Arg	Ser	Leu	Lys	Asn	Leu	Ile	Leu	Lys	Asn	Asn	Gln	Ile	Arg
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<213> Homo sapiens

<400> 37

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Met Val Phe Pro Met Trp Thr Leu Lys Arg Gln Ile Leu Ile Leu Phe
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Asn Ile Ile Leu Ile Ser Lys Leu Leu Gly Ala Arg Trp Phe Pro Lys
20           25           30

Thr Leu Pro Cys Asp Val Thr Leu Asp Val Pro Lys Asn His Val Ile
35           40           45

Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro Gly Gly Ile Pro
50           55           60

Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn His Ile Pro Asp Ile
65           70           75           80

Ser Pro Ala Ser Phe His Arg Leu Asp His Leu Val Glu Ile Asp Phe
85           90           95

Arg Cys Asn Cys Val Pro Ile Pro Leu Gly Ser Lys Asn Asn Met Cys
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Ile Lys Arg Leu Gln Ile Lys Pro Arg Ser Phe Ser Gly Leu Thr Tyr
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Leu Lys Ser Leu Tyr Leu Asp Gly Asn Gln Leu Leu Glu Ile Pro Gln
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Gly Leu Pro Pro Ser Leu Gln Leu Leu Ser Leu Glu Ala Asn Asn Ile
145          150          155          160

Phe Ser Ile Arg Lys Glu Asn Leu Thr Glu Leu Ala Asn Ile Glu Ile
165          170          175

Leu Tyr Leu Gly Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Tyr Val Ser
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Tyr Ser Ile Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val
195          200          205

Leu Ser Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro
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Ser Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile
225          230          235          240

Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp Leu
245          250          255

Ser Gly Asn Cys Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys Ala Pro
260          265          270

Cys Lys Asn Asn Ser Pro Leu Gln Ile Pro Val Asn Ala Phe Asp Ala
275          280          285

Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn Ser Leu Gln His
290          295          300

Val Pro Pro Arg Trp Phe Lys Asn Ile Asn Lys Leu Gln Glu Leu Asp
305          310          315          320

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Leu Ser Gln Asn Phe Leu Ala Lys Glu Ile Gly Asp Ala Lys Phe Leu
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 His Phe Leu Pro Ser Leu Ile Gln Leu Asp Leu Ser Phe Asn Phe Glu
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 Leu Gln Val Tyr Arg Ala Ser Met Asn Leu Ser Gln Ala Phe Ser Ser
 355 360 365
 Leu Lys Ser Leu Lys Ile Leu Arg Ile Arg Gly Tyr Val Phe Lys Glu
 370 375 380
 Leu Lys Ser Phe Asn Leu Ser Pro Leu His Asn Leu Gln Asn Leu Glu
 385 390 395 400
 Val Leu Asp Leu Gly Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met
 405 410 415
 Phe Lys Gln Phe Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys
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 Ile Ser Pro Ser Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala
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 Arg Thr Ser Val Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His
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 Tyr Phe Arg Tyr Asp Lys Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys
 465 470 475 480
 Glu Ala Ser Phe Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly Gln
 485 490 495
 Thr Leu Asp Leu Ser Lys Asn Ser Ile Phe Phe Val Lys Ser Ser Asp
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 Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser Gly Asn Leu
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 Ile Ser Gln Thr Leu Asn Gly Ser Glu Phe Gln Pro Leu Ala Glu Leu
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 Arg Tyr Leu Asp Phe Ser Asn Asn Arg Leu Asp Leu Leu His Ser Thr
 545 550 555 560
 Ala Phe Glu Glu Leu His Lys Leu Glu Val Leu Asp Ile Ser Ser Asn
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 Ser His Tyr Phe Gln Ser Glu Gly Ile Thr His Met Leu Asn Phe Thr
 580 585 590
 Lys Asn Leu Lys Val Leu Gln Lys Leu Met Met Asn Asp Asn Asp Ile
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 Ser Ser Ser Thr Ser Arg Thr Met Glu Ser Glu Ser Leu Arg Thr Leu
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 Glu Phe Arg Gly Asn His Leu Asp Val Leu Trp Arg Glu Gly Asp Asn
 625 630 635 640
 Arg Tyr Leu Gln Leu Phe Lys Asn Leu Leu Lys Leu Glu Glu Leu Asp

Ile	Ser	Lys	Asn	645	Ser	Leu	Ser	Phe	Leu	650	Pro	Ser	Gly	Val	Phe	655	Asp	Gly
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			675				680						685					
Ser	Phe	Ser	Trp	Lys	Lys	Leu	Gln	Cys	Leu	Lys	Asn	Leu	Glu	Thr	Leu			
	690					695					700							
Asp	Leu	Ser	His	Asn	Gln	Leu	Thr	Thr	Val	Pro	Glu	Arg	Leu	Ser	Asn			
705					710				715						720			
Cys	Ser	Arg	Ser	Leu	Lys	Asn	Leu	Ile	Leu	Lys	Asn	Asn	Gln	Ile	Arg			
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Ser	Leu	Thr	Lys	Tyr	Phe	Leu	Gln	Asp	Ala	Phe	Gln	Leu	Arg	Tyr	Leu			
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Asp	Leu	Ser	Ser	Asn	Lys	Ile	Gln	Met	Ile	Gln	Lys	Thr	Ser	Phe	Pro			
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Glu	Asn	Val	Leu	Asn	Asn	Leu	Lys	Met	Leu	Leu	Leu	His	His	Asn	Arg			
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Cys	Glu	Leu	Asp	Leu	Thr	Asn	Leu	Ile	Leu	Phe	Ser	Leu	Ser	Ile	Ser			
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Val	Ser	Leu	Phe	Leu	Met	Val	Met	Met	Thr	Ala	Ser	His	Leu	Tyr	Phe			
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 Thr Leu Pro Cys Glu Val Lys Val Asn Ile Pro Glu Ala His Val Ile
 35 40 45
 Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro Glu Gly Ile Pro
 50 55 60
 Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn His Ile Pro Ser Ile
 65 70 75 80
 Ser Pro Asp Ser Phe Arg Arg Leu Asn His Leu Glu Glu Ile Asp Leu
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 Arg Cys Asn Cys Val Pro Val Leu Leu Gly Ser Lys Ala Asn Val Cys
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 Thr Lys Arg Leu Gln Ile Arg Pro Gly Ser Phe Ser Gly Leu Ser Asp
 115 120 125
 Leu Lys Ala Leu Tyr Leu Asp Gly Asn Gln Leu Leu Glu Ile Pro Gln
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 Asp Leu Pro Ser Ser Leu His Leu Leu Ser Leu Glu Ala Asn Asn Ile
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 Phe Ser Ile Thr Lys Glu Asn Leu Thr Glu Leu Val Asn Ile Glu Thr
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 Leu Tyr Leu Gly Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Asn Val Ser
 180 185 190
 Tyr Ser Ile Glu Lys Asp Ala Phe Leu Val Met Arg Asn Leu Lys Val
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 Leu Ser Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Thr Leu Pro
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 Pro Asn Leu Leu Glu Leu Tyr Leu Tyr Asn Asn Ile Ile Lys Lys Ile

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Ser Gly Asn Cys Pro Arg Cys Tyr Asn Val Pro Tyr Pro Cys Thr Pro						
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Cys Glu Asn Asn Ser Pro Leu Gln Ile His Asp Asn Ala Phe Asn Ser						
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Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn Ser Leu Gln His						
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Val Pro Pro Thr Trp Phe Lys Asn Met Arg Asn Leu Gln Glu Leu Asp						
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Leu Ser Gln Asn Tyr Leu Ala Arg Glu Ile Glu Glu Ala Lys Phe Leu						
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His Phe Leu Pro Asn Leu Val Glu Leu Asp Phe Ser Phe Asn Tyr Glu						
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Leu Gln Val Tyr His Ala Ser Ile Thr Leu Pro His Ser Leu Ser Ser						
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Leu Glu Asn Leu Lys Ile Leu Arg Val Lys Gly Tyr Val Phe Lys Glu						
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Leu Lys Asn Ser Ser Leu Ser Val Leu His Lys Leu Pro Arg Leu Glu						
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Val Leu Asp Leu Gly Thr Asn Phe Ile Lys Ile Ala Asp Leu Asn Ile						
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Phe Lys His Phe Glu Asn Leu Lys Leu Ile Asp Leu Ser Val Asn Lys						
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Ile Ser Pro Ser Glu Glu Ser Arg Glu Val Gly Phe Cys Pro Asn Ala						
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Gln Thr Ser Val Asp Arg His Gly Pro Gln Val Leu Glu Ala Leu His						
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Tyr Phe Arg Tyr Asp Glu Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys						
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Glu Pro Pro Ser Phe Leu Pro Leu Asn Ala Asp Cys His Ile Tyr Gly						
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Gln Thr Leu Asp Leu Ser Arg Asn Asn Ile Phe Phe Ile Lys Pro Ser						
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Asp Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser Gly Asn						
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Thr Ile Gly Gln Thr Leu Asn Gly Ser Glu Leu Trp Pro Leu Arg Glu						
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Leu Arg Tyr Leu Asp Phe Ser Asn Asn Arg Leu Asp Leu Leu Tyr Ser						
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Thr Ala Phe Glu Glu Leu Gln Ser Leu Glu Val Leu Asp Leu Ser Ser						

Asn	Ser	His	Tyr	565	Phe	Gln	Ala	Glu	Gly	570	Ile	Thr	His	Met	Leu	575	Asn	Phe
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Thr	Lys	Lys	Leu	Arg	Leu	Leu	Asp	Lys	Leu	Met	Met	Asn	Asp	Asn	Asp			
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Ile	Ser	Thr	Ser	Ala	Ser	Arg	Thr	Met	Glu	Ser	Asp	Ser	Leu	Arg	Ile			
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Asp	Ile	Ser	Arg	Asn	Ser	Leu	Asn	Ser	Leu	Pro	Pro	Glu	Val	Phe	Glu			
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Asn	Cys	Ser	Lys	Ser	Leu	Thr	Thr	Leu	Ile	Leu	Lys	His	Asn	Gln	Ile			
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Arg	Gln	Leu	Thr	Lys	Tyr	Phe	Leu	Glu	Asp	Ala	Leu	Gln	Leu	Arg	Tyr			
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Pro	Glu	Asn	Val	Leu	Asn	Asn	Leu	Glu	Met	Leu	Val	Leu	His	His	Asn			
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Arg	Phe	Leu	Cys	Asn	Cys	Asp	Ala	Val	Trp	Phe	Val	Trp	Trp	Val	Asn			
785					790					795					800			
His	Thr	Asp	Val	Thr	Ile	Pro	Tyr	Leu	Ala	Thr	Asp	Val	Thr	Cys	Val			
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Thr	Cys	Glu	Leu	Asp	Leu	Thr	Asn	Leu	Ile	Leu	Phe	Ser	Val	Ser	Ile			
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Ser	Ser	Val	Leu	Phe	Leu	Met	Val	Val	Met	Thr	Thr	Ser	His	Leu	Phe			
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Phe	Trp	Asp	Met	Trp	Tyr	Ile	Tyr	Tyr	Phe	Trp	Lys	Ala	Lys	Ile	Lys			
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Gly	Tyr	Gln	His	Leu	Gln	Ser	Met	Glu	Ser	Cys	Tyr	Asp	Ala	Phe	Ile			
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Val	Tyr	Asp	Thr	Lys	Asn	Ser	Ala	Val	Thr	Glu	Trp	Val	Leu	Gln	Glu			

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 Lys Tyr Ala Lys Thr Glu Ser Phe Lys Met Ala Phe Tyr Leu Ser His
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 Gln Arg Leu Leu Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe Leu
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 Glu Lys Pro Leu Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg Leu
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 Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro Glu Gly Ile Pro
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 Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn His Ile Pro Ser Ile
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 Ser Pro Asp Ser Phe Arg Arg Leu Asn His Leu Glu Glu Ile Asp Leu
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 Arg Cys Asn Cys Val Pro Val Leu Leu Gly Ser Lys Ala Asn Val Cys
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 115 120 125
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 180 185 190
 Tyr Ser Ile Glu Lys Asp Ala Phe Leu Val Met Arg Asn Leu Lys Val
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 Pro Asn Leu Leu Glu Leu Tyr Leu Tyr Asn Asn Ile Ile Lys Lys Ile
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 Cys Glu Asn Asn Ser Pro Leu Gln Ile His Asp Asn Ala Phe Asn Ser
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Asp	Phe	Gln	His	Leu	Ser	Phe
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Asn	Cys	Ser	Lys	Ser	Leu	Thr
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Arg	Gln	Leu	Thr	Lys	Tyr	Phe
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Arg	Phe	Leu	Cys	Asn	Cys	Asp
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His	Thr	Asp	Val	Thr	Ile	Pro
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 Gly Pro Gly Ala His Lys Gly Gln Ser Val Ile Ser Leu Asp Leu Tyr
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 Thr Cys Glu Leu Asp Leu Thr Asn Leu Ile Leu Phe Ser Val Ser Ile
 835 840 845
 Ser Ser Val Leu Phe Leu Met Val Val Met Thr Thr Ser His Leu Phe
 850 855 860
 Phe Trp Asp Met Trp Tyr Ile Tyr Tyr Phe Trp Lys Ala Lys Ile Lys
 865 870 875 880
 Gly Tyr Gln His Leu Gln Ser Met Glu Ser Cys Tyr Asp Ala Phe Ile
 885 890 895
 Val Tyr Asp Thr Lys Asn Ser Ala Val Thr Glu Trp Val Leu Gln Glu
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 Ser Gln Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Gln
 945 950 955 960
 Lys Tyr Ala Lys Thr Glu Ser Phe Lys Met Ala Phe Tyr Leu Ser His
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 Gln Arg Leu Leu Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe Leu
 980 985 990
 Glu Lys Pro Leu Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg Leu
 995 1000 1005
 Cys Arg Ser Ser Val Leu Glu Trp Pro Ala Asn Pro Gln Ala His
 1010 1015 1020
 Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Thr Thr Asp Asn
 1025 1030 1035
 His Val Ala Tyr Ser Gln Met Phe Lys Glu Thr Val
 1040 1045 1050

<210> 43
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 <212> PRT
 <213> murine

<400> 43

Met Val Phe Ser Met Trp Thr Arg Lys Arg Gln Ile Leu Ile Phe Leu
 1 5 10 15
 Asn Met Leu Leu Val Ser Arg Val Phe Gly Phe Arg Trp Phe Pro Lys
 20 25 30
 Thr Leu Pro Cys Glu Val Lys Val Asn Ile Pro Glu Ala His Val Ile
 35 40 45

Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro Glu Gly Ile Pro
 50 55 60
 Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn His Ile Pro Ser Ile
 65 70 75 80
 Ser Pro Asp Ser Phe Arg Arg Leu Asn His Leu Glu Glu Ile Asp Leu
 85 90 95
 Arg Cys Asn Cys Val Pro Val Leu Leu Gly Ser Lys Ala Asn Val Cys
 100 105 110
 Thr Lys Arg Leu Gln Ile Arg Pro Gly Ser Phe Ser Gly Leu Ser Asp
 115 120 125
 Leu Lys Ala Leu Tyr Leu Asp Gly Asn Gln Leu Leu Glu Ile Pro Gln
 130 135 140
 Asp Leu Pro Ser Ser Leu His Leu Leu Ser Leu Glu Ala Asn Asn Ile
 145 150 155 160
 Phe Ser Ile Thr Lys Glu Asn Leu Thr Glu Leu Val Asn Ile Glu Thr
 165 170 175
 Leu Tyr Leu Gly Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Asn Val Ser
 180 185 190
 Tyr Ser Ile Glu Lys Asp Ala Phe Leu Val Met Arg Asn Leu Lys Val
 195 200 205
 Leu Ser Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Thr Leu Pro
 210 215 220
 Pro Asn Leu Leu Glu Leu Tyr Leu Tyr Asn Asn Ile Ile Lys Lys Ile
 225 230 235 240
 Gln Glu Asn Asp Phe Asn Asn Leu Asn Glu Leu Gln Val Leu Asp Leu
 245 250 255
 Ser Gly Asn Cys Pro Arg Cys Tyr Asn Val Pro Tyr Pro Cys Thr Pro
 260 265 270
 Cys Glu Asn Asn Ser Pro Leu Gln Ile His Asp Asn Ala Phe Asn Ser
 275 280 285
 Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn Ser Leu Gln His
 290 295 300
 Val Pro Pro Thr Trp Phe Lys Asn Met Arg Asn Leu Gln Glu Leu Asp
 305 310 315 320
 Leu Ser Gln Asn Tyr Leu Ala Arg Glu Ile Glu Glu Ala Lys Phe Leu
 325 330 335
 His Phe Leu Pro Asn Leu Val Glu Leu Asp Phe Ser Phe Asn Tyr Glu
 340 345 350
 Leu Gln Val Tyr His Ala Ser Ile Thr Leu Pro His Ser Leu Ser Ser
 355 360 365
 Leu Glu Asn Leu Lys Ile Leu Arg Val Lys Gly Tyr Val Phe Lys Glu

370	375	380																	
Leu Lys Asn Ser Ser	Leu Ser Val Leu His Lys	Leu Pro Arg Leu Glu																	
385	390	395																	400
Val Leu Asp Leu Gly Thr Asn Phe Ile Lys Ile Ala Asp Leu Asn Ile																			
	405	410																	415
Phe Lys His Phe Glu Asn Leu Lys Leu Ile Asp Leu Ser Val Asn Lys																			
	420	425																	430
Ile Ser Pro Ser Glu Glu Ser Arg Glu Val Gly Phe Cys Pro Asn Ala																			
	435	440																	445
Gln Thr Ser Val Asp Arg His Gly Pro Gln Val Leu Glu Ala Leu His																			
	450	455																	460
Tyr Phe Arg Tyr Asp Glu Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys																			
	465	470																	480
Glu Pro Pro Ser Phe Leu Pro Leu Asn Ala Asp Cys His Ile Tyr Gly																			
	485	490																	495
Gln Thr Leu Asp Leu Ser Arg Asn Asn Ile Phe Phe Ile Lys Pro Ser																			
	500	505																	510
Asp Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser Gly Asn																			
	515	520																	525
Thr Ile Gly Gln Thr Leu Asn Gly Ser Glu Leu Trp Pro Leu Arg Glu																			
	530	535																	540
Leu Arg Tyr Leu Asp Phe Ser Asn Asn Arg Leu Asp Leu Leu Tyr Ser																			
	545	550																	560
Thr Ala Phe Glu Glu Leu Gln Ser Leu Glu Val Leu Asp Leu Ser Ser																			
	565	570																	575
Asn Ser His Tyr Phe Gln Ala Glu Gly Ile Thr His Met Leu Asn Phe																			
	580	585																	590
Thr Lys Lys Leu Arg Leu Leu Asp Lys Leu Met Met Asn Asp Asn Asp																			
	595	600																	605
Ile Ser Thr Ser Ala Ser Arg Thr Met Glu Ser Asp Ser Leu Arg Ile																			
	610	615																	620
Leu Glu Phe Arg Gly Asn His Leu Asp Val Leu Trp Arg Ala Gly Asp																			
	625	630																	640
Asn Arg Tyr Leu Asp Phe Phe Lys Asn Leu Phe Asn Leu Glu Val Leu																			
	645	650																	655
Asp Ile Ser Arg Asn Ser Leu Asn Ser Leu Pro Pro Glu Val Phe Glu																			
	660	665																	670
Gly Met Pro Pro Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu																			
	675	680																	685
Lys Ser Phe Phe Trp Asp Arg Leu Gln Leu Leu Lys His Leu Glu Ile																			
	690	695																	700
Leu Asp Leu Ser His Asn Gln Leu Thr Lys Val Pro Glu Arg Leu Ala																			

705		710		715		720
Asn Cys Ser Lys	Ser Leu Thr Thr Leu Ile Leu Lys His Asn Gln Ile					
	725		730			735
Arg Gln Leu Thr Lys Tyr Phe Leu Glu Asp Ala Leu Gln Leu Arg Tyr						
	740		745			750
Leu Asp Ile Ser Ser Asn Lys Ile Gln Val Ile Gln Lys Thr Ser Phe						
	755		760			765
Pro Glu Asn Val Leu Asn Asn Leu Glu Met Leu Val Leu His His Asn						
	770		775			780
Arg Phe Leu Cys Asn Cys Asp Ala Val Trp Phe Val Trp Trp Val Asn						
	785		790			795
His Thr Asp Val Thr Ile Pro Tyr Leu Ala Thr Asp Val Thr Cys Val						
	805		810			815
Gly Pro Gly Ala His Lys Gly Gln Ser Val Ile Ser Leu Asp Leu Tyr						
	820		825			830
Thr Cys Glu Leu Asp Leu Thr Asn Leu Ile Leu Phe Ser Val Ser Ile						
	835		840			845
Ser Ser Val Leu Phe Leu Met Val Val Met Thr Thr Ser His Leu Phe						
	850		855			860
Phe Trp Asp Met Trp Tyr Ile Tyr Tyr Phe Trp Lys Ala Lys Ile Lys						
	865		870			875
Gly Tyr Gln His Leu Gln Ser Met Glu Ser Cys Tyr Asp Ala Phe Ile						
	885		890			895
Val Tyr Asp Thr Lys Asn Ser Ala Val Thr Glu Trp Val Leu Gln Glu						
	900		905			910
Leu Val Ala Lys Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys						
	915		920			925
Leu Glu Glu Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu						
	930		935			940
Ser Gln Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Gln						
	945		950			955
Lys Tyr Ala Lys Thr Glu Ser Phe Lys Met Ala Phe Tyr Leu Ser His						
	965		970			975
Gln Arg Leu Leu Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe Leu						
	980		985			990
Glu Lys Pro Leu Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg Leu						
	995		1000			1005
Cys Arg Ser Ser Val Leu Glu Trp Pro Ala Asn Pro Gln Ala His						
	1010		1015			1020
Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Thr Thr Asp Asn						
	1025		1030			1035
His Val Ala Tyr Ser Gln Met Phe Lys Glu Thr Val						

1040 1045 1050

<210> 44
 <211> 1050
 <212> PRT
 <213> murine

<400> 44

Met Val Phe Ser Met Trp Thr Arg Lys Arg Gln Ile Leu Ile Phe Leu
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Asn Met Leu Leu Val Ser Arg Val Phe Gly Phe Arg Trp Phe Pro Lys
 20 25 30

Thr Leu Pro Cys Glu Val Lys Val Asn Ile Pro Glu Ala His Val Ile
 35 40 45

Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro Glu Gly Ile Pro
 50 55 60

Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn His Ile Pro Ser Ile
 65 70 75 80

Ser Pro Asp Ser Phe Arg Arg Leu Asn His Leu Glu Glu Ile Asp Leu
 85 90 95

Arg Cys Asn Cys Val Pro Val Leu Leu Gly Ser Lys Ala Asn Val Cys
 100 105 110

Thr Lys Arg Leu Gln Ile Arg Pro Gly Ser Phe Ser Gly Leu Ser Asp
 115 120 125

Leu Lys Ala Leu Tyr Leu Asp Gly Asn Gln Leu Leu Glu Ile Pro Gln
 130 135 140

Asp Leu Pro Ser Ser Leu His Leu Leu Ser Leu Glu Ala Asn Asn Ile
 145 150 155 160

Phe Ser Ile Thr Lys Glu Asn Leu Thr Glu Leu Val Asn Ile Glu Thr
 165 170 175

Leu Tyr Leu Gly Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Asn Val Ser
 180 185 190

Tyr Ser Ile Glu Lys Asp Ala Phe Leu Val Met Arg Asn Leu Lys Val
 195 200 205

Leu Ser Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Thr Leu Pro
 210 215 220

Pro Asn Leu Leu Glu Leu Tyr Leu Tyr Asn Asn Ile Ile Lys Lys Ile
 225 230 235 240

Gln Glu Asn Asp Phe Asn Asn Leu Asn Glu Leu Gln Val Leu Asp Leu
 245 250 255

Ser Gly Asn Cys Pro Arg Cys Tyr Asn Val Pro Tyr Pro Cys Thr Pro
 260 265 270

Cys Glu Asn Asn Ser Pro Leu Gln Ile His Asp Asn Ala Phe Asn Ser
 275 280 285

Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn Ser Leu Gln His
 290 295 300
 Val Pro Pro Thr Trp Phe Lys Asn Met Arg Asn Leu Gln Glu Leu Asp
 305 310 315 320
 Leu Ser Gln Asn Tyr Leu Ala Arg Glu Ile Glu Glu Ala Lys Phe Leu
 325 330 335
 His Phe Leu Pro Asn Leu Val Glu Leu Asp Phe Ser Phe Asn Tyr Glu
 340 345 350
 Leu Gln Val Tyr His Ala Ser Ile Thr Leu Pro His Ser Leu Ser Ser
 355 360 365
 Leu Glu Asn Leu Lys Ile Leu Arg Val Lys Gly Tyr Val Phe Lys Glu
 370 375 380
 Leu Lys Asn Ser Ser Leu Ser Val Leu His Lys Leu Pro Arg Leu Glu
 385 390 395 400
 Val Leu Asp Leu Gly Thr Asn Phe Ile Lys Ile Ala Asp Leu Asn Ile
 405 410 415
 Phe Lys His Phe Glu Asn Leu Lys Leu Ile Asp Leu Ser Val Asn Lys
 420 425 430
 Ile Ser Pro Ser Glu Glu Ser Arg Glu Val Gly Phe Cys Pro Asn Ala
 435 440 445
 Gln Thr Ser Val Asp Arg His Gly Pro Gln Val Leu Glu Ala Leu His
 450 455 460
 Tyr Phe Arg Tyr Asp Glu Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys
 465 470 475 480
 Glu Pro Pro Ser Phe Leu Pro Leu Asn Ala Asp Cys His Ile Tyr Gly
 485 490 495
 Gln Thr Leu Asp Leu Ser Arg Asn Asn Ile Phe Phe Ile Lys Pro Ser
 500 505 510
 Asp Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser Gly Asn
 515 520 525
 Thr Ile Gly Gln Thr Leu Asn Gly Ser Glu Leu Trp Pro Leu Arg Glu
 530 535 540
 Leu Arg Tyr Leu Asp Phe Ser Asn Asn Arg Leu Asp Leu Leu Tyr Ser
 545 550 555 560
 Thr Ala Phe Glu Glu Leu Gln Ser Leu Glu Val Leu Asp Leu Ser Ser
 565 570 575
 Asn Ser His Tyr Phe Gln Ala Glu Gly Ile Thr His Met Leu Asn Phe
 580 585 590
 Thr Lys Lys Leu Arg Leu Leu Asp Lys Leu Met Met Asn Asp Asn Asp
 595 600 605
 Ile Ser Thr Ser Ala Ser Arg Thr Met Glu Ser Asp Ser Leu Arg Ile

610	615	620
Leu Glu Phe Arg Gly Asn His Leu Asp Val Leu Trp Arg Ala Gly Asp		
625	630	635 640
Asn Arg Tyr Leu Asp Phe Phe Lys Asn Leu Phe Asn Leu Glu Val Leu		
	645	650 655
Asp Ile Ser Arg Asn Ser Leu Asn Ser Leu Pro Pro Glu Val Phe Glu		
	660	665 670
Gly Met Pro Pro Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu		
	675	680 685
Lys Ser Phe Phe Trp Asp Arg Leu Gln Leu Leu Lys His Leu Glu Ile		
	690	695 700
Leu Asp Leu Ser His Asn Gln Leu Thr Lys Val Pro Glu Arg Leu Ala		
	705	710 715 720
Asn Cys Ser Lys Ser Leu Thr Thr Leu Ile Leu Lys His Asn Gln Ile		
	725	730 735
Arg Gln Leu Thr Lys Tyr Phe Leu Glu Asp Ala Leu Gln Leu Arg Tyr		
	740	745 750
Leu Asp Ile Ser Ser Asn Lys Ile Gln Val Ile Gln Lys Thr Ser Phe		
	755	760 765
Pro Glu Asn Val Leu Asn Asn Leu Glu Met Leu Val Leu His His Asn		
	770	775 780
Arg Phe Leu Cys Asn Cys Asp Ala Val Trp Phe Val Trp Trp Val Asn		
	785	790 795 800
His Thr Asp Val Thr Ile Pro Tyr Leu Ala Thr Asp Val Thr Cys Val		
	805	810 815
Gly Pro Gly Ala His Lys Gly Gln Ser Val Ile Ser Leu Asp Leu Tyr		
	820	825 830
Thr Cys Glu Leu Asp Leu Thr Asn Leu Ile Leu Phe Ser Val Ser Ile		
	835	840 845
Ser Ser Val Leu Phe Leu Met Val Val Met Thr Thr Ser His Leu Phe		
	850	855 860
Phe Trp Asp Met Trp Tyr Ile Tyr Tyr Phe Trp Lys Ala Lys Ile Lys		
	865	870 875 880
Gly Tyr Gln His Leu Gln Ser Met Glu Ser Cys Tyr Asp Ala Phe Ile		
	885	890 895
Val Tyr Asp Thr Lys Asn Ser Ala Val Thr Glu Trp Val Leu Gln Glu		
	900	905 910
Leu Val Ala Lys Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys		
	915	920 925
Leu Glu Glu Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu		
	930	935 940
Ser Gln Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Gln		

945 950 955 960
 Lys Tyr Ala Lys Thr Glu Ser Phe Lys Met Ala Phe Tyr Leu Ser His
 965 970 975

 Gln Arg Leu Leu Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe Leu
 980 985 990

 Glu Lys Pro Leu Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg Leu
 995 1000 1005

 Cys Arg Ser Ser Val Leu Glu Trp Pro Ala Asn Pro Gln Ala His
 1010 1015 1020

 Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Thr Thr Asp Asn
 1025 1030 1035

 His Val Ala Tyr Ser Gln Met Phe Lys Glu Thr Val
 1040 1045 1050

 <210> 45
 <211> 1050
 <212> PRT
 <213> murine

 <400> 45

 Met Val Phe Ser Met Trp Thr Arg Lys Arg Gln Ile Leu Ile Phe Leu
 1 5 10 15

 Asn Met Leu Leu Val Ser Arg Val Phe Gly Phe Arg Trp Phe Pro Lys
 20 25 30

 Thr Leu Pro Cys Glu Val Lys Val Asn Ile Pro Glu Ala His Val Ile
 35 40 45

 Val Asp Cys Thr Asp Lys His Leu Thr Glu Ile Pro Glu Gly Ile Pro
 50 55 60

 Thr Asn Thr Thr Asn Leu Thr Leu Thr Ile Asn His Ile Pro Ser Ile
 65 70 75 80

 Ser Pro Asp Ser Phe Arg Arg Leu Asn His Leu Glu Glu Ile Asp Leu
 85 90 95

 Arg Cys Asn Cys Val Pro Val Leu Leu Gly Ser Lys Ala Asn Val Cys
 100 105 110

 Thr Lys Arg Leu Gln Ile Arg Pro Gly Ser Phe Ser Gly Leu Ser Asp
 115 120 125

 Leu Lys Ala Leu Tyr Leu Asp Gly Asn Gln Leu Leu Glu Ile Pro Gln
 130 135 140

 Asp Leu Pro Ser Ser Leu His Leu Leu Ser Leu Glu Ala Asn Asn Ile
 145 150 155 160

 Phe Ser Ile Thr Lys Glu Asn Leu Thr Glu Leu Val Asn Ile Glu Thr
 165 170 175

 Leu Tyr Leu Gly Gln Asn Cys Tyr Tyr Arg Asn Pro Cys Asn Val Ser
 180 185 190

Tyr Ser Ile Glu Lys Asp Ala Phe Leu Val Met Arg Asn Leu Lys Val
 195 200 205
 Leu Ser Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Thr Leu Pro
 210 215 220
 Pro Asn Leu Leu Glu Leu Tyr Leu Tyr Asn Asn Ile Ile Lys Lys Ile
 225 230 235 240
 Gln Glu Asn Asp Phe Asn Asn Leu Asn Glu Leu Gln Val Leu Asp Leu
 245 250 255
 Ser Gly Asn Cys Pro Arg Cys Tyr Asn Val Pro Tyr Pro Cys Thr Pro
 260 265 270
 Cys Glu Asn Asn Ser Pro Leu Gln Ile His Asp Asn Ala Phe Asn Ser
 275 280 285
 Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn Ser Leu Gln His
 290 295 300
 Val Pro Pro Thr Trp Phe Lys Asn Met Arg Asn Leu Gln Glu Leu Asp
 305 310 315 320
 Leu Ser Gln Asn Tyr Leu Ala Arg Glu Ile Glu Glu Ala Lys Phe Leu
 325 330 335
 His Phe Leu Pro Asn Leu Val Glu Leu Asp Phe Ser Phe Asn Tyr Glu
 340 345 350
 Leu Gln Val Tyr His Ala Ser Ile Thr Leu Pro His Ser Leu Ser Ser
 355 360 365
 Leu Glu Asn Leu Lys Ile Leu Arg Val Lys Gly Tyr Val Phe Lys Glu
 370 375 380
 Leu Lys Asn Ser Ser Leu Ser Val Leu His Lys Leu Pro Arg Leu Glu
 385 390 395 400
 Val Leu Asp Leu Gly Thr Asn Phe Ile Lys Ile Ala Asp Leu Asn Ile
 405 410 415
 Phe Lys His Phe Glu Asn Leu Lys Leu Ile Asp Leu Ser Val Asn Lys
 420 425 430
 Ile Ser Pro Ser Glu Glu Ser Arg Glu Val Gly Phe Cys Pro Asn Ala
 435 440 445
 Gln Thr Ser Val Asp Arg His Gly Pro Gln Val Leu Glu Ala Leu His
 450 455 460
 Tyr Phe Arg Tyr Asp Glu Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys
 465 470 475 480
 Glu Pro Pro Ser Phe Leu Pro Leu Asn Ala Asp Cys His Ile Tyr Gly
 485 490 495
 Gln Thr Leu Asp Leu Ser Arg Asn Asn Ile Phe Phe Ile Lys Pro Ser
 500 505 510
 Asp Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser Gly Asn

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Thr	Ile	Gly	Gln	Thr	Leu	Asn	Gly	Ser	Glu	Leu	Trp	Pro	Leu	Arg	Glu	
	530					535					540					
Leu	Arg	Tyr	Leu	Asp	Phe	Ser	Asn	Asn	Arg	Leu	Asp	Leu	Leu	Tyr	Ser	
545					550					555					560	
Thr	Ala	Phe	Glu	Glu	Leu	Gln	Ser	Leu	Glu	Val	Leu	Asp	Leu	Ser	Ser	
				565					570					575		
Asn	Ser	His	Tyr	Phe	Gln	Ala	Glu	Gly	Ile	Thr	His	Met	Leu	Asn	Phe	
			580					585					590			
Thr	Lys	Lys	Leu	Arg	Leu	Leu	Asp	Lys	Leu	Met	Met	Asn	Asp	Asn	Asp	
		595					600					605				
Ile	Ser	Thr	Ser	Ala	Ser	Arg	Thr	Met	Glu	Ser	Asp	Ser	Leu	Arg	Ile	
	610					615					620					
Leu	Glu	Phe	Arg	Gly	Asn	His	Leu	Asp	Val	Leu	Trp	Arg	Ala	Gly	Asp	
625					630					635					640	
Asn	Arg	Tyr	Leu	Asp	Phe	Phe	Lys	Asn	Leu	Phe	Asn	Leu	Glu	Val	Leu	
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Asp	Ile	Ser	Arg	Asn	Ser	Leu	Asn	Ser	Leu	Pro	Pro	Glu	Val	Phe	Glu	
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Gly	Met	Pro	Pro	Asn	Leu	Lys	Asn	Leu	Ser	Leu	Ala	Lys	Asn	Gly	Leu	
		675					680					685				
Lys	Ser	Phe	Phe	Trp	Asp	Arg	Leu	Gln	Leu	Leu	Lys	His	Leu	Glu	Ile	
	690					695					700					
Leu	Asp	Leu	Ser	His	Asn	Gln	Leu	Thr	Lys	Val	Pro	Glu	Arg	Leu	Ala	
705					710					715					720	
Asn	Cys	Ser	Lys	Ser	Leu	Thr	Thr	Leu	Ile	Leu	Lys	His	Asn	Gln	Ile	
				725					730					735		
Arg	Gln	Leu	Thr	Lys	Tyr	Phe	Leu	Glu	Asp	Ala	Leu	Gln	Leu	Arg	Tyr	
			740					745					750			
Leu	Asp	Ile	Ser	Ser	Asn	Lys	Ile	Gln	Val	Ile	Gln	Lys	Thr	Ser	Phe	
		755					760					765				
Pro	Glu	Asn	Val	Leu	Asn	Asn	Leu	Glu	Met	Leu	Val	Leu	His	His	Asn	
	770					775					780					
Arg	Phe	Leu	Cys	Asn	Cys	Asp	Ala	Val	Trp	Phe	Val	Trp	Trp	Val	Asn	
785					790					795					800	
His	Thr	Asp	Val	Thr	Ile	Pro	Tyr	Leu	Ala	Thr	Asp	Val	Thr	Cys	Val	
				805					810					815		
Gly	Pro	Gly	Ala	His	Lys	Gly	Gln	Ser	Val	Ile	Ser	Leu	Asp	Leu	Tyr	
			820				825						830			
Thr	Cys	Glu	Leu	Asp	Leu	Thr	Asn	Leu	Ile	Leu	Phe	Ser	Val	Ser	Ile	
		835					840					845				
Ser	Ser	Val	Leu	Phe	Leu	Met	Val	Val	Met	Thr	Thr	Ser	His	Leu	Phe	

850 855 860
 Phe Trp Asp Met Trp Tyr Ile Tyr Tyr Phe Trp Lys Ala Lys Ile Lys
 865 870 875 880
 Gly Tyr Gln His Leu Gln Ser Met Glu Ser Cys Tyr Asp Ala Phe Ile
 885 890 895
 Val Tyr Asp Thr Lys Asn Ser Ala Val Thr Glu Trp Val Leu Gln Glu
 900 905 910
 Leu Val Ala Lys Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys
 915 920 925
 Leu Glu Glu Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu
 930 935 940
 Ser Gln Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Gln
 945 950 955 960
 Lys Tyr Ala Lys Thr Glu Ser Phe Lys Met Ala Phe Tyr Leu Ser His
 965 970 975
 Gln Arg Leu Leu Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe Leu
 980 985 990
 Glu Lys Pro Leu Gln Lys Ser Lys Phe Leu Gln Leu Arg Lys Arg Leu
 995 1000 1005
 Cys Arg Ser Ser Val Leu Glu Trp Pro Ala Asn Pro Gln Ala His
 1010 1015 1020
 Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Thr Thr Asp Asn
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 His Val Ala Tyr Ser Gln Met Phe Lys Glu Thr Val
 1040 1045 1050

<210> 46

<211> 3311

<212> DNA

<213> Homo sapiens

<400> 46

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tcttttaact	atataaaggg	gagttatcca	cagcatatta	atatttccag	aaacttctct	1140
aaacttttgt	ctctacgggc	attgcattta	agaggttatg	tgttccagga	actcagagaa	1200
gatgatttcc	agccctgat	gcagcttcca	aacttatcga	ctatcaactt	gggtattaat	1260
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ttgtcagaaa	acagaatatc	accgttggtg	aaagataccc	ggcagagtta	tgcaaatagt	1380
tcctcttttc	aacgtcatat	ccggaaacga	cgctcaacag	attttgagtt	tgaccacat	1440
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gccttagatt	taagcctcaa	cagtattttc	ttcattgggc	caaaccaatt	tgaaaatctt	1560
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Ser Tyr Pro Cys Asp Glu Lys Lys Gln Asn Asp Ser Val Ile Ala Glu
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 Cys Ser Asn Arg Arg Leu Gln Glu Val Pro Gln Thr Val Gly Lys Tyr
 50 55 60
 Val Thr Glu Leu Asp Leu Ser Asp Asn Phe Ile Thr His Ile Thr Asn
 65 70 75 80
 Glu Ser Phe Gln Gly Leu Gln Asn Leu Thr Lys Ile Asn Leu Asn His
 85 90 95
 Asn Pro Asn Val Gln His Gln Asn Gly Asn Pro Gly Ile Gln Ser Asn
 100 105 110
 Gly Leu Asn Ile Thr Asp Gly Ala Phe Leu Asn Leu Lys Asn Leu Arg
 115 120 125
 Glu Leu Leu Leu Glu Asp Asn Gln Leu Pro Gln Ile Pro Ser Gly Leu
 130 135 140
 Pro Glu Ser Leu Thr Glu Leu Ser Leu Ile Gln Asn Asn Ile Tyr Asn
 145 150 155 160
 Ile Thr Lys Glu Gly Ile Ser Arg Leu Ile Asn Leu Lys Asn Leu Tyr
 165 170 175
 Leu Ala Trp Asn Cys Tyr Phe Asn Lys Val Cys Glu Lys Thr Asn Ile
 180 185 190
 Glu Asp Gly Val Phe Glu Thr Leu Thr Asn Leu Glu Leu Leu Ser Leu
 195 200 205
 Ser Phe Asn Ser Leu Ser His Val Pro Pro Lys Leu Pro Ser Ser Leu
 210 215 220
 Arg Lys Leu Phe Leu Ser Asn Thr Gln Ile Lys Tyr Ile Ser Glu Glu
 225 230 235 240
 Asp Phe Lys Gly Leu Ile Asn Leu Thr Leu Leu Asp Leu Ser Gly Asn
 245 250 255
 Cys Pro Arg Cys Phe Asn Ala Pro Phe Pro Cys Val Pro Cys Asp Gly
 260 265 270
 Gly Ala Ser Ile Asn Ile Asp Arg Phe Ala Phe Gln Asn Leu Thr Gln
 275 280 285
 Leu Arg Tyr Leu Asn Leu Ser Ser Thr Ser Leu Arg Lys Ile Asn Ala
 290 295 300
 Ala Trp Phe Lys Asn Met Pro His Leu Lys Val Leu Asp Leu Glu Phe
 305 310 315 320
 Asn Tyr Leu Val Gly Glu Ile Ala Ser Gly Ala Phe Leu Thr Met Leu
 325 330 335
 Pro Arg Leu Glu Ile Leu Asp Leu Ser Phe Asn Tyr Ile Lys Gly Ser
 340 345 350
 Tyr Pro Gln His Ile Asn Ile Ser Arg Asn Phe Ser Lys Leu Leu Ser

355	360	365
Leu Arg Ala Leu His Leu Arg Gly Tyr Val Phe Gln Glu Leu Arg Glu		
370	375	380
Asp Asp Phe Gln Pro Leu Met Gln Leu Pro Asn Leu Ser Thr Ile Asn		
385	390	395 400
Leu Gly Ile Asn Phe Ile Lys Gln Ile Asp Phe Lys Leu Phe Gln Asn		
	405	410 415
Phe Ser Asn Leu Glu Ile Ile Tyr Leu Ser Glu Asn Arg Ile Ser Pro		
	420	425 430
Leu Val Lys Asp Thr Arg Gln Ser Tyr Ala Asn Ser Ser Ser Phe Gln		
	435	440 445
Arg His Ile Arg Lys Arg Arg Ser Thr Asp Phe Glu Phe Asp Pro His		
	450	455 460
Ser Asn Phe Tyr His Phe Thr Arg Pro Leu Ile Lys Pro Gln Cys Ala		
	465	470 475 480
Ala Tyr Gly Lys Ala Leu Asp Leu Ser Leu Asn Ser Ile Phe Phe Ile		
	485	490 495
Gly Pro Asn Gln Phe Glu Asn Leu Pro Asp Ile Ala Cys Leu Asn Leu		
	500	505 510
Ser Ala Asn Ser Asn Ala Gln Val Leu Ser Gly Thr Glu Phe Ser Ala		
	515	520 525
Ile Pro His Val Lys Tyr Leu Asp Leu Thr Asn Asn Arg Leu Asp Phe		
	530	535 540
Asp Asn Ala Ser Ala Leu Thr Glu Leu Ser Asp Leu Glu Val Leu Asp		
	545	550 555 560
Leu Ser Tyr Asn Ser His Tyr Phe Arg Ile Ala Gly Val Thr His His		
	565	570 575
Leu Glu Phe Ile Gln Asn Phe Thr Asn Leu Lys Val Leu Asn Leu Ser		
	580	585 590
His Asn Asn Ile Tyr Thr Leu Thr Asp Lys Tyr Asn Leu Glu Ser Lys		
	595	600 605
Ser Leu Val Glu Leu Val Phe Ser Gly Asn Arg Leu Asp Ile Leu Trp		
	610	615 620
Asn Asp Asp Asp Asn Arg Tyr Ile Ser Ile Phe Lys Gly Leu Lys Asn		
	625	630 635 640
Leu Thr Arg Leu Asp Leu Ser Leu Asn Arg Leu Lys His Ile Pro Asn		
	645	650 655
Glu Ala Phe Leu Asn Leu Pro Ala Ser Leu Thr Glu Leu His Ile Asn		
	660	665 670
Asp Asn Met Leu Lys Phe Phe Asn Trp Thr Leu Leu Gln Gln Phe Pro		
	675	680 685
Arg Leu Glu Leu Leu Asp Leu Arg Gly Asn Lys Leu Leu Phe Leu Thr		

690	695	700
Asp Ser Leu Ser Asp Phe Thr Ser Ser Leu Arg Thr Leu Leu Leu Ser		
705	710	715 720
His Asn Arg Ile Ser His Leu Pro Ser Gly Phe Leu Ser Glu Val Ser		
	725	730 735
Ser Leu Lys His Leu Asp Leu Ser Ser Asn Leu Leu Lys Thr Ile Asn		
	740	745 750
Lys Ser Ala Leu Glu Thr Lys Thr Thr Thr Lys Leu Ser Met Leu Glu		
	755	760 765
Leu His Gly Asn Pro Phe Glu Cys Thr Cys Asp Ile Gly Asp Phe Arg		
	770	775 780
Arg Trp Met Asp Glu His Leu Asn Val Lys Ile Pro Arg Leu Val Asp		
	785	790 795 800
Val Ile Cys Ala Ser Pro Gly Asp Gln Arg Gly Lys Ser Ile Val Ser		
	805	810 815
Leu Glu Leu Thr Thr Cys Val Ser Asp Val Thr Ala Val Ile Leu Phe		
	820	825 830
Phe Phe Thr Phe Phe Ile Thr Thr Met Val Met Leu Ala Ala Leu Ala		
	835	840 845
His His Leu Phe Tyr Trp Asp Val Trp Phe Ile Tyr Asn Val Cys Leu		
	850	855 860
Ala Lys Val Lys Gly Tyr Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr		
	865	870 875 880
Asp Ala Tyr Ile Ser Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp		
	885	890 895
Val Ile Asn Glu Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn		
	900	905 910
Val Leu Leu Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile		
	915	920 925
Ile Asp Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe		
	930	935 940
Val Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe		
	945	950 955 960
Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile Ile		
	965	970 975
Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu Arg Leu		
	980	985 990
Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro Asp Asn Pro		
	995	1000 1005
Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn Val Val Leu		
	1010	1015 1020
Thr Glu Asn Asp Ser Arg Tyr Asn Asn Met Tyr Val Asp Ser Ile		

1025
Lys Gln Tyr
1040

1030

1035

<210> 51
<211> 1059
<212> PRT
<213> Homo sapiens

<400> 51

Met Lys Glu Ser Ser Leu Gln Asn Ser Ser Cys Ser Leu Gly Lys Glu
1 5 10 15

Thr Lys Lys Glu Asn Met Phe Leu Gln Ser Ser Met Leu Thr Cys Ile
20 25 30

Phe Leu Leu Ile Ser Gly Ser Cys Glu Leu Cys Ala Glu Glu Asn Phe
35 40 45

Ser Arg Ser Tyr Pro Cys Asp Glu Lys Lys Gln Asn Asp Ser Val Ile
50 55 60

Ala Glu Cys Ser Asn Arg Arg Leu Gln Glu Val Pro Gln Thr Val Gly
65 70 75 80

Lys Tyr Val Thr Glu Leu Asp Leu Ser Asp Asn Phe Ile Thr His Ile
85 90 95

Thr Asn Glu Ser Phe Gln Gly Leu Gln Asn Leu Thr Lys Ile Asn Leu
100 105 110

Asn His Asn Pro Asn Val Gln His Gln Asn Gly Asn Pro Gly Ile Gln
115 120 125

Ser Asn Gly Leu Asn Ile Thr Asp Gly Ala Phe Leu Asn Leu Lys Asn
130 135 140

Leu Arg Glu Leu Leu Leu Glu Asp Asn Gln Leu Pro Gln Ile Pro Ser
145 150 155 160

Gly Leu Pro Glu Ser Leu Thr Glu Leu Ser Leu Ile Gln Asn Asn Ile
165 170 175

Tyr Asn Ile Thr Lys Glu Gly Ile Ser Arg Leu Ile Asn Leu Lys Asn
180 185 190

Leu Tyr Leu Ala Trp Asn Cys Tyr Phe Asn Lys Val Cys Glu Lys Thr
195 200 205

Asn Ile Glu Asp Gly Val Phe Glu Thr Leu Thr Asn Leu Glu Leu Leu
210 215 220

Ser Leu Ser Phe Asn Ser Leu Ser His Val Ser Pro Lys Leu Pro Ser
225 230 235 240

Ser Leu Arg Lys Leu Phe Leu Ser Asn Thr Gln Ile Lys Tyr Ile Ser
245 250 255

Glu Glu Asp Phe Lys Gly Leu Ile Asn Leu Thr Leu Leu Asp Leu Ser
260 265 270

Gly Asn Cys Pro Arg Cys Phe Asn Ala Pro Phe Pro Cys Val Pro Cys
 275 280 285
 Asp Gly Gly Ala Ser Ile Asn Ile Asp Arg Phe Ala Phe Gln Asn Leu
 290 295 300
 Thr Gln Leu Arg Tyr Leu Asn Leu Ser Ser Thr Ser Leu Arg Lys Ile
 305 310 315 320
 Asn Ala Ala Trp Phe Lys Asn Met Pro His Leu Lys Val Leu Asp Leu
 325 330 335
 Glu Phe Asn Tyr Leu Val Gly Glu Ile Ala Ser Gly Ala Phe Leu Thr
 340 345 350
 Met Leu Pro Arg Leu Glu Ile Leu Asp Leu Ser Phe Asn Tyr Ile Lys
 355 360 365
 Gly Ser Tyr Pro Gln His Ile Asn Ile Ser Arg Asn Phe Ser Lys Pro
 370 375 380
 Leu Ser Leu Arg Ala Leu His Leu Arg Gly Tyr Val Phe Gln Glu Leu
 385 390 395 400
 Arg Glu Asp Asp Phe Gln Pro Leu Met Gln Leu Pro Asn Leu Ser Thr
 405 410 415
 Ile Asn Leu Gly Ile Asn Phe Ile Lys Gln Ile Asp Phe Lys Leu Phe
 420 425 430
 Gln Asn Phe Ser Asn Leu Glu Ile Ile Tyr Leu Ser Glu Asn Arg Ile
 435 440 445
 Ser Pro Leu Val Lys Asp Thr Arg Gln Ser Tyr Ala Asn Ser Ser Ser
 450 455 460
 Phe Gln Arg His Ile Arg Lys Arg Arg Ser Thr Asp Phe Glu Phe Asp
 465 470 475 480
 Pro His Ser Asn Phe Tyr His Phe Thr Arg Pro Leu Ile Lys Pro Gln
 485 490 495
 Cys Ala Ala Tyr Gly Lys Ala Leu Asp Leu Ser Leu Asn Ser Ile Phe
 500 505 510
 Phe Ile Gly Pro Asn Gln Phe Glu Asn Leu Pro Asp Ile Ala Cys Leu
 515 520 525
 Asn Leu Ser Ala Asn Ser Asn Ala Gln Val Leu Ser Gly Thr Glu Phe
 530 535 540
 Ser Ala Ile Pro His Val Lys Tyr Leu Asp Leu Thr Asn Asn Arg Leu
 545 550 555 560
 Asp Phe Asp Asn Ala Ser Ala Leu Thr Glu Leu Ser Asp Leu Glu Val
 565 570 575
 Leu Asp Leu Ser Tyr Asn Ser His Tyr Phe Arg Ile Ala Gly Val Thr
 580 585 590
 His His Leu Glu Phe Ile Gln Asn Phe Thr Asn Leu Lys Val Leu Asn

595	600	605
Leu Ser His Asn Asn Ile Tyr Thr Leu Thr Asp Lys Tyr Asn Leu Glu		
610	615	620
Ser Lys Ser Leu Val Glu Leu Val Phe Ser Gly Asn Arg Leu Asp Ile		
625	630	635 640
Leu Trp Asn Asp Asp Asp Asn Arg Tyr Ile Ser Ile Phe Lys Gly Leu		
	645	650 655
Lys Asn Leu Thr Arg Leu Asp Leu Ser Leu Asn Arg Leu Lys His Ile		
	660	665 670
Pro Asn Glu Ala Phe Leu Asn Leu Pro Ala Ser Leu Thr Glu Leu His		
	675	680 685
Ile Asn Asp Asn Met Leu Lys Phe Phe Asn Trp Thr Leu Leu Gln Gln		
	690	695 700
Phe Pro Arg Leu Glu Leu Leu Asp Leu Arg Gly Asn Lys Leu Leu Phe		
705	710	715 720
Leu Thr Asp Ser Leu Ser Asp Phe Thr Ser Ser Leu Arg Thr Leu Leu		
	725	730 735
Leu Ser His Asn Arg Ile Ser His Leu Pro Ser Gly Phe Leu Ser Glu		
	740	745 750
Val Ser Ser Leu Lys His Leu Asp Leu Ser Ser Asn Leu Leu Lys Thr		
	755	760 765
Ile Asn Lys Ser Ala Leu Glu Thr Lys Thr Thr Thr Lys Leu Ser Met		
	770	775 780
Leu Glu Leu His Gly Asn Pro Phe Glu Cys Thr Cys Asp Ile Gly Asp		
785	790	795 800
Phe Arg Arg Trp Met Asp Glu His Leu Asn Val Lys Ile Pro Arg Leu		
	805	810 815
Val Asp Val Ile Cys Ala Ser Pro Gly Asp Gln Arg Gly Lys Ser Ile		
	820	825 830
Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp Val Thr Ala Val Ile		
	835	840 845
Leu Phe Phe Phe Thr Phe Phe Ile Thr Thr Met Val Met Leu Ala Ala		
	850	855 860
Leu Ala His His Leu Phe Tyr Trp Asp Val Trp Phe Ile Tyr Asn Val		
865	870	875 880
Cys Leu Ala Lys Ile Lys Gly Tyr Arg Ser Leu Ser Thr Ser Gln Thr		
	885	890 895
Phe Tyr Asp Ala Tyr Ile Ser Tyr Asp Thr Lys Asp Ala Ser Val Thr		
	900	905 910
Asp Trp Val Ile Asn Glu Leu Arg Tyr His Leu Glu Glu Ser Arg Asp		
	915	920 925
Lys Asn Val Leu Leu Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu		

930 935 940
 Ala Ile Ile Asp Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr
 945 950 955 960
 Val Phe Val Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr
 965 970 975
 Ala Phe Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val
 980 985 990
 Ile Ile Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu
 995 1000 1005
 Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro
 1010 1015 1020
 Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn
 1025 1030 1035
 Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asn Asn Met Tyr Val
 1040 1045 1050
 Asp Ser Ile Lys Gln Tyr
 1055

<210> 52
 <211> 1041
 <212> PRT
 <213> Homo sapiens

<400> 52

Met Glu Asn Met Phe Leu Gln Ser Ser Met Leu Thr Cys Ile Phe Leu
 1 5 10 15
 Leu Ile Ser Gly Ser Cys Glu Leu Cys Ala Glu Glu Asn Phe Ser Arg
 20 25 30
 Ser Tyr Pro Cys Asp Glu Lys Lys Gln Asn Asp Ser Val Ile Ala Glu
 35 40 45
 Cys Ser Asn Arg Arg Leu Gln Glu Val Pro Gln Thr Val Gly Lys Tyr
 50 55 60
 Val Thr Glu Leu Asp Leu Ser Asp Asn Phe Ile Thr His Ile Thr Asn
 65 70 75 80
 Glu Ser Phe Gln Gly Leu Gln Asn Leu Thr Lys Ile Asn Leu Asn His
 85 90 95
 Asn Pro Asn Val Gln His Gln Asn Gly Asn Pro Gly Ile Gln Ser Asn
 100 105 110
 Gly Leu Asn Ile Thr Asp Gly Ala Phe Leu Asn Leu Lys Asn Leu Arg
 115 120 125
 Glu Leu Leu Leu Glu Asp Asn Gln Leu Pro Gln Ile Pro Ser Gly Leu
 130 135 140
 Pro Glu Ser Leu Thr Glu Leu Ser Leu Ile Gln Asn Asn Ile Tyr Asn
 145 150 155 160

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Ile Thr Lys Glu Gly Ile Ser Arg Leu Ile Asn Leu Lys Asn Leu Tyr
      165                      170                      175

Leu Ala Trp Asn Cys Tyr Phe Asn Lys Val Cys Glu Lys Thr Asn Ile
      180                      185                      190

Glu Asp Gly Val Phe Glu Thr Leu Thr Asn Leu Glu Leu Leu Ser Leu
      195                      200                      205

Ser Phe Asn Ser Leu Ser His Val Pro Pro Lys Leu Pro Ser Ser Leu
      210                      215                      220

Arg Lys Leu Phe Leu Ser Asn Thr Gln Ile Lys Tyr Ile Ser Glu Glu
      225                      230                      235                      240

Asp Phe Lys Gly Leu Ile Asn Leu Thr Leu Leu Asp Leu Ser Gly Asn
      245                      250                      255

Cys Pro Arg Cys Phe Asn Ala Pro Phe Pro Cys Val Pro Cys Asp Gly
      260                      265                      270

Gly Ala Ser Ile Asn Ile Asp Arg Phe Ala Phe Gln Asn Leu Thr Gln
      275                      280                      285

Leu Arg Tyr Leu Asn Leu Ser Ser Thr Ser Leu Arg Lys Ile Asn Ala
      290                      295                      300

Ala Trp Phe Lys Asn Met Pro His Leu Lys Val Leu Asp Leu Glu Phe
      305                      310                      315                      320

Asn Tyr Leu Val Gly Glu Ile Ala Ser Gly Ala Phe Leu Thr Met Leu
      325                      330                      335

Pro Arg Leu Glu Ile Leu Asp Leu Ser Phe Asn Tyr Ile Lys Gly Ser
      340                      345                      350

Tyr Pro Gln His Ile Asn Ile Ser Arg Asn Phe Ser Lys Leu Leu Ser
      355                      360                      365

Leu Arg Ala Leu His Leu Arg Gly Tyr Val Phe Gln Glu Leu Arg Glu
      370                      375                      380

Asp Asp Phe Gln Pro Leu Met Gln Leu Pro Asn Leu Ser Thr Ile Asn
      385                      390                      395                      400

Leu Gly Ile Asn Phe Ile Lys Gln Ile Asp Phe Lys Leu Phe Gln Asn
      405                      410                      415

Phe Ser Asn Leu Glu Ile Ile Tyr Leu Ser Glu Asn Arg Ile Ser Pro
      420                      425                      430

Leu Val Lys Asp Thr Arg Gln Ser Tyr Ala Asn Ser Ser Ser Phe Gln
      435                      440                      445

Arg His Ile Arg Lys Arg Arg Ser Thr Asp Phe Glu Phe Asp Pro His
      450                      455                      460

Ser Asn Phe Tyr His Phe Thr Arg Pro Leu Ile Lys Pro Gln Cys Ala
      465                      470                      475                      480

Ala Tyr Gly Lys Ala Leu Asp Leu Ser Leu Asn Ser Ile Phe Phe Ile

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	Gly	Pro	Asn	Gln 500	Phe	Glu	Asn	Leu	Pro 505	Asp	Ile	Ala	Cys	Leu 510	Asn	Leu
	Ser	Ala	Asn 515	Ser	Asn	Ala	Gln	Val 520	Leu	Ser	Gly	Thr	Glu 525	Phe	Ser	Ala
	Ile	Pro 530	His	Val	Lys	Tyr	Leu 535	Asp	Leu	Thr	Asn	Asn 540	Arg	Leu	Asp	Phe
	Asp 545	Asn	Ala	Ser	Ala	Leu 550	Thr	Glu	Leu	Ser	Asp 555	Leu	Glu	Val	Leu	Asp 560
	Leu	Ser	Tyr	Asn	Ser 565	His	Tyr	Phe	Arg	Ile 570	Ala	Gly	Val	Thr	His 575	His
	Leu	Glu	Phe	Ile 580	Gln	Asn	Phe	Thr	Asn 585	Leu	Lys	Val	Leu	Asn 590	Leu	Ser
	His	Asn	Asn 595	Ile	Tyr	Thr	Leu	Thr 600	Asp	Lys	Tyr	Asn	Leu 605	Glu	Ser	Lys
	Ser	Leu 610	Val	Glu	Leu	Val	Phe 615	Ser	Gly	Asn	Arg	Leu 620	Asp	Ile	Leu	Trp
	Asn 625	Asp	Asp	Asp	Asn 630	Arg	Tyr	Ile	Ser	Ile	Phe 635	Lys	Gly	Leu	Lys	Asn 640
	Leu	Thr	Arg	Leu	Asp 645	Leu	Ser	Leu	Asn	Arg 650	Leu	Lys	His	Ile	Pro 655	Asn
	Glu	Ala	Phe	Leu 660	Asn	Leu	Pro	Ala	Ser 665	Leu	Thr	Glu	Leu	His 670	Ile	Asn
	Asp	Asn	Met 675	Leu	Lys	Phe	Phe	Asn 680	Trp	Thr	Leu	Leu	Gln 685	Gln	Phe	Pro
	Arg 690	Leu	Glu	Leu	Leu	Asp	Leu 695	Arg	Gly	Asn	Lys	Leu 700	Leu	Phe	Leu	Thr
	Asp 705	Ser	Leu	Ser	Asp	Phe 710	Thr	Ser	Ser	Leu	Arg 715	Thr	Leu	Leu	Leu	Ser 720
	His	Asn	Arg	Ile	Ser 725	His	Leu	Pro	Ser	Gly 730	Phe	Leu	Ser	Glu 735	Val	Ser
	Ser	Leu	Lys	His 740	Leu	Asp	Leu	Ser	Ser 745	Asn	Leu	Leu	Lys	Thr 750	Ile	Asn
	Lys	Ser	Ala 755	Leu	Glu	Thr	Lys	Thr 760	Thr	Thr	Lys	Leu	Ser 765	Met	Leu	Glu
	Leu	His 770	Gly	Asn	Pro	Phe	Glu 775	Cys	Thr	Cys	Asp	Ile 780	Gly	Asp	Phe	Arg
	Arg 785	Trp	Met	Asp	Glu	His 790	Leu	Asn	Val	Lys	Ile 795	Pro	Arg	Leu	Val	Asp 800
	Val	Ile	Cys	Ala	Ser 805	Pro	Gly	Asp	Gln	Arg 810	Gly	Lys	Ser	Ile 815	Val	Ser
	Leu	Glu	Leu	Thr	Thr	Cys	Val	Ser	Asp	Val	Thr	Ala	Val	Ile	Leu	Phe

820 825 830
 Phe Phe Thr Phe Phe Ile Thr Thr Met Val Met Leu Ala Ala Leu Ala
 835 840 845
 His His Leu Phe Tyr Trp Asp Val Trp Phe Ile Tyr Asn Val Cys Leu
 850 855 860
 Ala Lys Val Lys Gly Tyr Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr
 865 870 875 880
 Asp Ala Tyr Ile Ser Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp
 885 890 895
 Val Ile Asn Glu Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn
 900 905 910
 Val Leu Leu Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile
 915 920 925
 Ile Asp Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe
 930 935 940
 Val Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe
 945 950 955 960
 Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile Ile
 965 970 975
 Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu Arg Leu
 980 985 990
 Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro Asp Asn Pro
 995 1000 1005
 Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn Val Val Leu
 1010 1015 1020
 Thr Glu Asn Asp Ser Arg Tyr Asn Asn Met Tyr Val Asp Ser Ile
 1025 1030 1035
 Lys Gln Tyr
 1040

<210> 53
 <211> 1041
 <212> PRT
 <213> Homo sapiens

<400> 53

Met Glu Asn Met Phe Leu Gln Ser Ser Met Leu Thr Cys Ile Phe Leu
 1 5 10 15
 Leu Ile Ser Gly Ser Cys Glu Leu Cys Ala Glu Glu Asn Phe Ser Arg
 20 25 30
 Ser Tyr Pro Cys Asp Glu Lys Lys Gln Asn Asp Ser Val Ile Ala Glu
 35 40 45
 Cys Ser Asn Arg Arg Leu Gln Glu Val Pro Gln Thr Val Gly Lys Tyr
 50 55 60

Val	Thr	Glu	Leu	Asp	Leu	Ser	Asp	Asn	Phe	Ile	Thr	His	Ile	Thr	Asn	65	70	75	80
Glu	Ser	Phe	Gln	Gly	Leu	Gln	Asn	Leu	Thr	Lys	Ile	Asn	Leu	Asn	His	85	90	95	
Asn	Pro	Asn	Val	Gln	His	Gln	Asn	Gly	Asn	Pro	Gly	Ile	Gln	Ser	Asn	100	105	110	
Gly	Leu	Asn	Ile	Thr	Asp	Gly	Ala	Phe	Leu	Asn	Leu	Lys	Asn	Leu	Arg	115	120	125	
Glu	Leu	Leu	Leu	Glu	Asp	Asn	Gln	Leu	Pro	Gln	Ile	Pro	Ser	Gly	Leu	130	135	140	
Pro	Glu	Ser	Leu	Thr	Glu	Leu	Ser	Leu	Ile	Gln	Asn	Asn	Ile	Tyr	Asn	145	150	155	160
Ile	Thr	Lys	Glu	Gly	Ile	Ser	Arg	Leu	Ile	Asn	Leu	Lys	Asn	Leu	Tyr	165	170	175	
Leu	Ala	Trp	Asn	Cys	Tyr	Phe	Asn	Lys	Val	Cys	Glu	Lys	Thr	Asn	Ile	180	185	190	
Glu	Asp	Gly	Val	Phe	Glu	Thr	Leu	Thr	Asn	Leu	Glu	Leu	Leu	Ser	Leu	195	200	205	
Ser	Phe	Asn	Ser	Leu	Ser	His	Val	Pro	Pro	Lys	Leu	Pro	Ser	Ser	Leu	210	215	220	
Arg	Lys	Leu	Phe	Leu	Ser	Asn	Thr	Gln	Ile	Lys	Tyr	Ile	Ser	Glu	Glu	225	230	235	240
Asp	Phe	Lys	Gly	Leu	Ile	Asn	Leu	Thr	Leu	Leu	Asp	Leu	Ser	Gly	Asn	245	250	255	
Cys	Pro	Arg	Cys	Phe	Asn	Ala	Pro	Phe	Pro	Cys	Val	Pro	Cys	Asp	Gly	260	265	270	
Gly	Ala	Ser	Ile	Asn	Ile	Asp	Arg	Phe	Ala	Phe	Gln	Asn	Leu	Thr	Gln	275	280	285	
Leu	Arg	Tyr	Leu	Asn	Leu	Ser	Ser	Thr	Ser	Leu	Arg	Lys	Ile	Asn	Ala	290	295	300	
Ala	Trp	Phe	Lys	Asn	Met	Pro	His	Leu	Lys	Val	Leu	Asp	Leu	Glu	Phe	305	310	315	320
Asn	Tyr	Leu	Val	Gly	Glu	Ile	Ala	Ser	Gly	Ala	Phe	Leu	Thr	Met	Leu	325	330	335	
Pro	Arg	Leu	Glu	Ile	Leu	Asp	Leu	Ser	Phe	Asn	Tyr	Ile	Lys	Gly	Ser	340	345	350	
Tyr	Pro	Gln	His	Ile	Asn	Ile	Ser	Arg	Asn	Phe	Ser	Lys	Leu	Leu	Ser	355	360	365	
Leu	Arg	Ala	Leu	His	Leu	Arg	Gly	Tyr	Val	Phe	Gln	Glu	Leu	Arg	Glu	370	375	380	
Asp	Asp	Phe	Gln	Pro	Leu	Met	Gln	Leu	Pro	Asn	Leu	Ser	Thr	Ile	Asn				

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Ser	Leu	Lys	His	Leu	Asp	Leu	Ser	Ser	Asn	Leu	Leu	Lys	Thr	Ile	Asn
			740					745					750		
Lys	Ser	Ala	Leu	Glu	Thr	Lys	Thr	Thr	Thr	Lys	Leu	Ser	Met	Leu	Glu
		755					760					765			
Leu	His	Gly	Asn	Pro	Phe	Glu	Cys	Thr	Cys	Asp	Ile	Gly	Asp	Phe	Arg
	770					775					780				
Arg	Trp	Met	Asp	Glu	His	Leu	Asn	Val	Lys	Ile	Pro	Arg	Leu	Val	Asp
785					790					795					800
Val	Ile	Cys	Ala	Ser	Pro	Gly	Asp	Gln	Arg	Gly	Lys	Ser	Ile	Val	Ser
				805					810					815	
Leu	Glu	Leu	Thr	Thr	Cys	Val	Ser	Asp	Val	Thr	Ala	Val	Ile	Leu	Phe
			820					825					830		
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Asp	Ala	Tyr	Ile	Ser	Tyr	Asp	Thr	Lys	Asp	Ala	Ser	Val	Thr	Asp	Trp
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Val	Leu	Thr	Lys	Lys	Tyr	Ala	Lys	Ser	Trp	Asn	Phe	Lys	Thr	Ala	Phe
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Phe Leu Leu Ile Ser Gly Ser Cys Glu Leu Cys Ala Glu Glu Asn Phe
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Ser Arg Ser Tyr Pro Cys Asp Glu Lys Lys Gln Asn Asp Ser Val Ile
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Lys Tyr Val Thr Glu Leu Asp Leu Ser Asp Asn Phe Ile Thr His Ile
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Thr Asn Glu Ser Phe Gln Gly Leu Gln Asn Leu Thr Lys Ile Asn Leu
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Ser Leu Arg Lys Leu Phe Leu Ser Asn Thr Gln Ile Lys Tyr Ile Ser
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Glu Glu Asp Phe Lys Gly Leu Ile Asn Leu Thr Leu Leu Asp Leu Ser
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Gly Asn Cys Pro Arg Cys Phe Asn Ala Pro Phe Pro Cys Val Pro Cys
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Leu Trp Asn Asp Asp Asp Asn Arg Tyr Ile Ser Ile Phe Lys Gly Leu		
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3220

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Ser	Tyr	Pro	Cys	Asp	Glu	Ile	Arg	His	Asn	Ser	Leu	Val	Ile	Ala	Glu	35	40	45	
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Val	Thr	Asn	Ile	Asp	Leu	Ser	Asp	Asn	Ala	Ile	Thr	His	Ile	Thr	Lys	65	70	75	80
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Phe	Tyr	Val	Pro	Pro	Lys	Leu	Pro	Ser	Ser	Leu	Arg	Lys	Leu	Phe	Leu	210	215	220	
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Glu	Asn	Leu	Thr	Leu	Leu	Asp	Leu	Ser	Gly	Asn	Cys	Pro	Arg	Cys	Tyr	245	250	255	
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 Leu Asp Leu Ser Phe Asn Phe Gln Tyr Lys Glu Tyr Leu Gln Phe Ile
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 Asn Ile Ser Ser Asn Phe Ser Lys Leu Arg Ser Leu Lys Lys Leu His
 355 360 365
 Leu Arg Gly Tyr Val Phe Arg Glu Leu Lys Lys Lys His Phe Glu His
 370 375 380
 Leu Gln Ser Leu Pro Asn Leu Ala Thr Ile Asn Leu Gly Ile Asn Phe
 385 390 395 400
 Ile Glu Lys Ile Asp Phe Lys Ala Phe Gln Asn Phe Ser Lys Leu Asp
 405 410 415
 Val Ile Tyr Leu Ser Gly Asn Arg Ile Ala Ser Val Leu Asp Gly Thr
 420 425 430
 Asp Tyr Ser Ser Trp Arg Asn Arg Leu Arg Lys Pro Leu Ser Thr Asp
 435 440 445
 Asp Asp Glu Phe Asp Pro His Val Asn Phe Tyr His Ser Thr Lys Pro
 450 455 460
 Leu Ile Lys Pro Gln Cys Thr Ala Tyr Gly Lys Ala Leu Asp Leu Ser
 465 470 475 480
 Leu Asn Asn Ile Phe Ile Ile Gly Lys Ser Gln Phe Glu Gly Phe Gln
 485 490 495
 Asp Ile Ala Cys Leu Asn Leu Ser Phe Asn Ala Asn Thr Gln Val Phe
 500 505 510
 Asn Gly Thr Glu Phe Ser Ser Met Pro His Ile Lys Tyr Leu Asp Leu
 515 520 525
 Thr Asn Asn Arg Leu Asp Phe Asp Asp Asn Asn Ala Phe Ser Asp Leu
 530 535 540
 His Asp Leu Glu Val Leu Asp Leu Ser His Asn Ala His Tyr Phe Ser
 545 550 555 560
 Ile Ala Gly Val Thr His Arg Leu Gly Phe Ile Gln Asn Leu Ile Asn
 565 570 575
 Leu Arg Val Leu Asn Leu Ser His Asn Gly Ile Tyr Thr Leu Thr Glu
 580 585 590
 Glu Ser Glu Leu Lys Ser Ile Ser Leu Lys Glu Leu Val Phe Ser Gly

595	600	605
Asn Arg Leu Asp His Leu Trp	Asn Ala Asn Asp Gly Lys Tyr Trp Ser	
610	615	620
Ile Phe Lys Ser Leu Gln Asn Leu Ile Arg Leu Asp Leu Ser Tyr Asn		
625	630	635
Asn Leu Gln Gln Ile Pro Asn Gly Ala Phe Leu Asn Leu Pro Gln Ser		
	645	650
Leu Gln Glu Leu Leu Ile Ser Gly Asn Lys Leu Arg Phe Phe Asn Trp		
	660	665
Thr Leu Leu Gln Tyr Phe Pro His Leu His Leu Leu Asp Leu Ser Arg		
	675	680
Asn Glu Leu Tyr Phe Leu Pro Asn Cys Leu Ser Lys Phe Ala His Ser		
	690	695
Leu Glu Thr Leu Leu Leu Ser His Asn His Phe Ser His Leu Pro Ser		
	705	710
Gly Phe Leu Ser Glu Ala Arg Asn Leu Val His Leu Asp Leu Ser Phe		
	725	730
Asn Thr Ile Lys Met Ile Asn Lys Ser Ser Leu Gln Thr Lys Met Lys		
	740	745
Thr Asn Leu Ser Ile Leu Glu Leu His Gly Asn Tyr Phe Asp Cys Thr		
	755	760
Cys Asp Ile Ser Asp Phe Arg Ser Trp Leu Asp Glu Asn Leu Asn Ile		
	770	775
Thr Ile Pro Lys Leu Val Asn Val Ile Cys Ser Asn Pro Gly Asp Gln		
	785	790
Lys Ser Lys Ser Ile Met Ser Leu Asp Leu Thr Thr Cys Val Ser Asp		
	805	810
Thr Thr Ala Ala Val Leu Phe Phe Leu Thr Phe Leu Thr Thr Ser Met		
	820	825
Val Met Leu Ala Ala Leu Val His His Leu Phe Tyr Trp Asp Val Trp		
	835	840
Phe Ile Tyr His Met Cys Ser Ala Lys Leu Lys Gly Tyr Arg Thr Ser		
	850	855
Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser Tyr Asp Thr Lys		
	865	870
Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu Leu Arg Tyr His Leu		
	885	890
Glu Glu Ser Glu Asp Lys Ser Val Leu Leu Cys Leu Glu Glu Arg Asp		
	900	905
Trp Asp Pro Gly Leu Pro Ile Ile Asp Asn Leu Met Gln Ser Ile Asn		
	915	920
Gln Ser Lys Lys Thr Ile Phe Val Leu Thr Lys Lys Tyr Ala Lys Ser		

930 935 940
 Trp Asn Phe Lys Thr Ala Phe Tyr Leu Ala Leu Gln Arg Leu Met Asp
 945 950 955 960

 Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu Glu Pro Val Leu Gln
 965 970 975

 Tyr Ser Gln Tyr Leu Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile
 980 985 990

 Leu Gln Trp Pro Asn Asn Pro Lys Ala Glu Asn Leu Phe Trp Gln Ser
 995 1000 1005

 Leu Lys Asn Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asp Asp
 1010 1015 1020

 Leu Tyr Ile Asp Ser Ile Arg Gln Tyr
 1025 1030

<210> 58
 <211> 1032
 <212> PRT
 <213> murine

<400> 58

Met Glu Asn Met Pro Pro Gln Ser Trp Ile Leu Thr Cys Phe Cys Leu
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 Leu Ser Ser Gly Thr Ser Ala Ile Phe His Lys Ala Asn Tyr Ser Arg
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 Ser Tyr Pro Cys Asp Glu Ile Arg His Asn Ser Leu Val Ile Ala Glu
 35 40 45

 Cys Asn His Arg Gln Leu His Glu Val Pro Gln Thr Ile Gly Lys Tyr
 50 55 60

 Val Thr Asn Ile Asp Leu Ser Asp Asn Ala Ile Thr His Ile Thr Lys
 65 70 75 80

 Glu Ser Phe Gln Lys Leu Gln Asn Leu Thr Lys Ile Asp Leu Asn His
 85 90 95

 Asn Ala Lys Gln Gln His Pro Asn Glu Asn Lys Asn Gly Met Asn Ile
 100 105 110

 Thr Glu Gly Ala Leu Leu Ser Leu Arg Asn Leu Thr Val Leu Leu Leu
 115 120 125

 Glu Asp Asn Gln Leu Tyr Thr Ile Pro Ala Gly Leu Pro Glu Ser Leu
 130 135 140

 Lys Glu Leu Ser Leu Ile Gln Asn Asn Ile Phe Gln Val Thr Lys Asn
 145 150 155 160

 Asn Thr Phe Gly Leu Arg Asn Leu Glu Arg Leu Tyr Leu Gly Trp Asn
 165 170 175

 Cys Tyr Phe Lys Cys Asn Gln Thr Phe Lys Val Glu Asp Gly Ala Phe
 180 185 190

Lys Asn Leu Ile His Leu Lys Val Leu Ser Leu Ser Phe Asn Asn Leu
 195 200 205
 Phe Tyr Val Pro Pro Lys Leu Pro Ser Ser Leu Arg Lys Leu Phe Leu
 210 215 220
 Ser Asn Ala Lys Ile Met Asn Ile Thr Gln Glu Asp Phe Lys Gly Leu
 225 230 235 240
 Glu Asn Leu Thr Leu Leu Asp Leu Ser Gly Asn Cys Pro Arg Cys Tyr
 245 250 255
 Asn Ala Pro Phe Pro Cys Thr Pro Cys Lys Glu Asn Ser Ser Ile His
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 Ile His Pro Leu Ala Phe Gln Ser Leu Thr Gln Leu Leu Tyr Leu Asn
 275 280 285
 Leu Ser Ser Thr Ser Leu Arg Thr Ile Pro Ser Thr Trp Phe Glu Asn
 290 295 300
 Leu Ser Asn Leu Lys Glu Leu His Leu Glu Phe Asn Tyr Leu Val Gln
 305 310 315 320
 Glu Ile Ala Ser Gly Ala Phe Leu Thr Lys Leu Pro Ser Leu Gln Ile
 325 330 335
 Leu Asp Leu Ser Phe Asn Phe Gln Tyr Lys Glu Tyr Leu Gln Phe Ile
 340 345 350
 Asn Ile Ser Ser Asn Phe Ser Lys Leu Arg Ser Leu Lys Lys Leu His
 355 360 365
 Leu Arg Gly Tyr Val Phe Arg Glu Leu Lys Lys Lys His Phe Glu His
 370 375 380
 Leu Gln Ser Leu Pro Asn Leu Ala Thr Ile Asn Leu Gly Ile Asn Phe
 385 390 395 400
 Ile Glu Lys Ile Asp Phe Lys Ala Phe Gln Asn Phe Ser Lys Leu Asp
 405 410 415
 Val Ile Tyr Leu Ser Gly Asn Arg Ile Ala Ser Val Leu Asp Gly Thr
 420 425 430
 Asp Tyr Ser Ser Trp Arg Asn Arg Leu Arg Lys Pro Leu Ser Thr Asp
 435 440 445
 Asp Asp Glu Phe Asp Pro His Val Asn Phe Tyr His Ser Thr Lys Pro
 450 455 460
 Leu Ile Lys Pro Gln Cys Thr Ala Tyr Gly Lys Ala Leu Asp Leu Ser
 465 470 475 480
 Leu Asn Asn Ile Phe Ile Ile Gly Lys Ser Gln Phe Glu Gly Phe Gln
 485 490 495
 Asp Ile Ala Cys Leu Asn Leu Ser Phe Asn Ala Asn Thr Gln Val Phe
 500 505 510
 Asn Gly Thr Glu Phe Ser Ser Met Pro His Ile Lys Tyr Leu Asp Leu

515	520	525
Thr Asn Asn Arg Leu Asp Phe Asp Asp Asn Asn Ala Phe Ser Asp Leu		
530	535	540
His Asp Leu Glu Val Leu Asp Leu Ser His Asn Ala His Tyr Phe Ser		
545	550	555
560		
Ile Ala Gly Val Thr His Arg Leu Gly Phe Ile Gln Asn Leu Ile Asn		
565	570	575
Leu Arg Val Leu Asn Leu Ser His Asn Gly Ile Tyr Thr Leu Thr Glu		
580	585	590
Glu Ser Glu Leu Lys Ser Ile Ser Leu Lys Glu Leu Val Phe Ser Gly		
595	600	605
Asn Arg Leu Asp His Leu Trp Asn Ala Asn Asp Gly Lys Tyr Trp Ser		
610	615	620
Ile Phe Lys Ser Leu Gln Asn Leu Ile Arg Leu Asp Leu Ser Tyr Asn		
625	630	635
640		
Asn Leu Gln Gln Ile Pro Asn Gly Ala Phe Leu Asn Leu Pro Gln Ser		
645	650	655
Leu Gln Glu Leu Leu Ile Ser Gly Asn Lys Leu Arg Phe Phe Asn Trp		
660	665	670
Thr Leu Leu Gln Tyr Phe Pro His Leu His Leu Leu Asp Leu Ser Arg		
675	680	685
Asn Glu Leu Tyr Phe Leu Pro Asn Cys Leu Ser Lys Phe Ala His Ser		
690	695	700
Leu Glu Thr Leu Leu Leu Ser His Asn His Phe Ser His Leu Pro Ser		
705	710	715
720		
Gly Phe Leu Ser Glu Ala Arg Asn Leu Val His Leu Asp Leu Ser Phe		
725	730	735
Asn Thr Ile Lys Met Ile Asn Lys Ser Ser Leu Gln Thr Lys Met Lys		
740	745	750
Thr Asn Leu Ser Ile Leu Glu Leu His Gly Asn Tyr Phe Asp Cys Thr		
755	760	765
Cys Asp Ile Ser Asp Phe Arg Ser Trp Leu Asp Glu Asn Leu Asn Ile		
770	775	780
Thr Ile Pro Lys Leu Val Asn Val Ile Cys Ser Asn Pro Gly Asp Gln		
785	790	795
800		
Lys Ser Lys Ser Ile Met Ser Leu Asp Leu Thr Thr Cys Val Ser Asp		
805	810	815
Thr Thr Ala Ala Val Leu Phe Phe Leu Thr Phe Leu Thr Thr Ser Met		
820	825	830
Val Met Leu Ala Ala Leu Val His His Leu Phe Tyr Trp Asp Val Trp		
835	840	845
Phe Ile Tyr His Met Cys Ser Ala Lys Leu Lys Gly Tyr Arg Thr Ser		

850 855 860
 Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser Tyr Asp Thr Lys
 865 870 875 880
 Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu Leu Arg Tyr His Leu
 885 890 895
 Glu Glu Ser Glu Asp Lys Ser Val Leu Leu Cys Leu Glu Glu Arg Asp
 900 905 910
 Trp Asp Pro Gly Leu Pro Ile Ile Asp Asn Leu Met Gln Ser Ile Asn
 915 920 925
 Gln Ser Lys Lys Thr Ile Phe Val Leu Thr Lys Lys Tyr Ala Lys Ser
 930 935 940
 Trp Asn Phe Lys Thr Ala Phe Tyr Leu Ala Leu Gln Arg Leu Met Asp
 945 950 955 960
 Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu Glu Pro Val Leu Gln
 965 970 975
 Tyr Ser Gln Tyr Leu Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile
 980 985 990
 Leu Gln Trp Pro Asn Asn Pro Lys Ala Glu Asn Leu Phe Trp Gln Ser
 995 1000 1005
 Leu Lys Asn Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asp Asp
 1010 1015 1020
 Leu Tyr Ile Asp Ser Ile Arg Gln Tyr
 1025 1030

<210> 59
 <211> 1032
 <212> PRT
 <213> murine

<400> 59

Met Glu Asn Met Pro Pro Gln Ser Trp Ile Leu Thr Cys Phe Cys Leu
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 Leu Ser Ser Gly Thr Ser Ala Ile Phe His Lys Ala Asn Tyr Ser Arg
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 Ser Tyr Pro Cys Asp Glu Ile Arg His Asn Ser Leu Val Ile Ala Glu
 35 40 45
 Cys Asn His Arg Gln Leu His Glu Val Pro Gln Thr Ile Gly Lys Tyr
 50 55 60
 Val Thr Asn Ile Asp Leu Ser Asp Asn Ala Ile Thr His Ile Thr Lys
 65 70 75 80
 Glu Ser Phe Gln Lys Leu Gln Asn Leu Thr Lys Ile Asp Leu Asn His
 85 90 95
 Asn Ala Lys Gln Gln His Pro Asn Glu Asn Lys Asn Gly Met Asn Ile
 100 105 110

Thr Glu Gly Ala Leu Leu Ser Leu Arg Asn Leu Thr Val Leu Leu Leu
 115 120 125
 Glu Asp Asn Gln Leu Tyr Thr Ile Pro Ala Gly Leu Pro Glu Ser Leu
 130 135 140
 Lys Glu Leu Ser Leu Ile Gln Asn Asn Ile Phe Gln Val Thr Lys Asn
 145 150 155 160
 Asn Thr Phe Gly Leu Arg Asn Leu Glu Arg Leu Tyr Leu Gly Trp Asn
 165 170 175
 Cys Tyr Phe Lys Cys Asn Gln Thr Phe Lys Val Glu Asp Gly Ala Phe
 180 185 190
 Lys Asn Leu Ile His Leu Lys Val Leu Ser Leu Ser Phe Asn Asn Leu
 195 200 205
 Phe Tyr Val Pro Pro Lys Leu Pro Ser Ser Leu Arg Lys Leu Phe Leu
 210 215 220
 Ser Asn Ala Lys Ile Met Asn Ile Thr Gln Glu Asp Phe Lys Gly Leu
 225 230 235 240
 Glu Asn Leu Thr Leu Leu Asp Leu Ser Gly Asn Cys Pro Arg Cys Tyr
 245 250 255
 Asn Ala Pro Phe Pro Cys Thr Pro Cys Lys Glu Asn Ser Ser Ile His
 260 265 270
 Ile His Pro Leu Ala Phe Gln Ser Leu Thr Gln Leu Leu Tyr Leu Asn
 275 280 285
 Leu Ser Ser Thr Ser Leu Arg Thr Ile Pro Ser Thr Trp Phe Glu Asn
 290 295 300
 Leu Ser Asn Leu Lys Glu Leu His Leu Glu Phe Asn Tyr Leu Val Gln
 305 310 315 320
 Glu Ile Ala Ser Gly Ala Phe Leu Thr Lys Leu Pro Ser Leu Gln Ile
 325 330 335
 Leu Asp Leu Ser Phe Asn Phe Gln Tyr Lys Glu Tyr Leu Gln Phe Ile
 340 345 350
 Asn Ile Ser Ser Asn Phe Ser Lys Leu Arg Ser Leu Lys Lys Leu His
 355 360 365
 Leu Arg Gly Tyr Val Phe Arg Glu Leu Lys Lys Lys His Phe Glu His
 370 375 380
 Leu Gln Ser Leu Pro Asn Leu Ala Thr Ile Asn Leu Gly Ile Asn Phe
 385 390 395 400
 Ile Glu Lys Ile Asp Phe Lys Ala Phe Gln Asn Phe Ser Lys Leu Asp
 405 410 415
 Val Ile Tyr Leu Ser Gly Asn Arg Ile Ala Ser Val Leu Asp Gly Thr
 420 425 430
 Asp Tyr Ser Ser Trp Arg Asn Arg Leu Arg Lys Pro Leu Ser Thr Asp

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Asp	Asp	Glu	Phe	Asp	Pro	His	Val	Asn	Phe	Tyr	His	Ser	Thr	Lys	Pro	
	450					455					460					
Leu	Ile	Lys	Pro	Gln	Cys	Thr	Ala	Tyr	Gly	Lys	Ala	Leu	Asp	Leu	Ser	
465					470					475						480
Leu	Asn	Asn	Ile	Phe	Ile	Ile	Gly	Lys	Ser	Gln	Phe	Glu	Gly	Phe	Gln	
				485					490					495		
Asp	Ile	Ala	Cys	Leu	Asn	Leu	Ser	Phe	Asn	Ala	Asn	Thr	Gln	Val	Phe	
			500					505					510			
Asn	Gly	Thr	Glu	Phe	Ser	Ser	Met	Pro	His	Ile	Lys	Tyr	Leu	Asp	Leu	
		515					520					525				
Thr	Asn	Asn	Arg	Leu	Asp	Phe	Asp	Asp	Asn	Asn	Ala	Phe	Ser	Asp	Leu	
	530					535					540					
His	Asp	Leu	Glu	Val	Leu	Asp	Leu	Ser	His	Asn	Ala	His	Tyr	Phe	Ser	
545					550					555					560	
Ile	Ala	Gly	Val	Thr	His	Arg	Leu	Gly	Phe	Ile	Gln	Asn	Leu	Ile	Asn	
				565					570					575		
Leu	Arg	Val	Leu	Asn	Leu	Ser	His	Asn	Gly	Ile	Tyr	Thr	Leu	Thr	Glu	
			580					585					590			
Glu	Ser	Glu	Leu	Lys	Ser	Ile	Ser	Leu	Lys	Glu	Leu	Val	Phe	Ser	Gly	
		595					600					605				
Asn	Arg	Leu	Asp	His	Leu	Trp	Asn	Ala	Asn	Asp	Gly	Lys	Tyr	Trp	Ser	
	610					615					620					
Ile	Phe	Lys	Ser	Leu	Gln	Asn	Leu	Ile	Arg	Leu	Asp	Leu	Ser	Tyr	Asn	
625					630					635					640	
Asn	Leu	Gln	Gln	Ile	Pro	Asn	Gly	Ala	Phe	Leu	Asn	Leu	Pro	Gln	Ser	
				645					650					655		
Leu	Gln	Glu	Leu	Leu	Ile	Ser	Gly	Asn	Lys	Leu	Arg	Phe	Phe	Asn	Trp	
			660					665					670			
Thr	Leu	Leu	Gln	Tyr	Phe	Pro	His	Leu	His	Leu	Leu	Asp	Leu	Ser	Arg	
		675					680					685				
Asn	Glu	Leu	Tyr	Phe	Leu	Pro	Asn	Cys	Leu	Ser	Lys	Phe	Ala	His	Ser	
	690					695					700					
Leu	Glu	Thr	Leu	Leu	Leu	Ser	His	Asn	His	Phe	Ser	His	Leu	Pro	Ser	
705					710					715					720	
Gly	Phe	Leu	Ser	Glu	Ala	Arg	Asn	Leu	Val	His	Leu	Asp	Leu	Ser	Phe	
				725					730					735		
Asn	Thr	Ile	Lys	Met	Ile	Asn	Lys	Ser	Ser	Leu	Gln	Thr	Lys	Met	Lys	
			740					745					750			
Thr	Asn	Leu	Ser	Ile	Leu	Glu	Leu	His	Gly	Asn	Tyr	Phe	Asp	Cys	Thr	
		755														

770 775 780
 Thr Ile Pro Lys Leu Val Asn Val Ile Cys Ser Asn Pro Gly Asp Gln
 785 790 795 800
 Lys Ser Lys Ser Ile Met Ser Leu Asp Leu Thr Thr Cys Val Ser Asp
 805 810 815
 Thr Thr Ala Ala Val Leu Phe Phe Leu Thr Phe Leu Thr Thr Ser Met
 820 825 830
 Val Met Leu Ala Ala Leu Val His His Leu Phe Tyr Trp Asp Val Trp
 835 840 845
 Phe Ile Tyr His Met Cys Ser Ala Lys Leu Lys Gly Tyr Arg Thr Ser
 850 855 860
 Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser Tyr Asp Thr Lys
 865 870 875 880
 Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu Leu Arg Tyr His Leu
 885 890 895
 Glu Glu Ser Glu Asp Lys Ser Val Leu Leu Cys Leu Glu Glu Arg Asp
 900 905 910
 Trp Asp Pro Gly Leu Pro Ile Ile Asp Asn Leu Met Gln Ser Ile Asn
 915 920 925
 Gln Ser Lys Lys Thr Ile Phe Val Leu Thr Lys Lys Tyr Ala Lys Ser
 930 935 940
 Trp Asn Phe Lys Thr Ala Phe Tyr Leu Ala Leu Gln Arg Leu Met Asp
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 Glu Asn Met Asp Val Ile Ile Phe Ile Leu Leu Glu Pro Val Leu Gln
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 Tyr Ser Gln Tyr Leu Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile
 980 985 990
 Leu Gln Trp Pro Asn Asn Pro Lys Ala Glu Asn Leu Phe Trp Gln Ser
 995 1000 1005
 Leu Lys Asn Val Val Leu Thr Glu Asn Asp Ser Arg Tyr Asp Asp
 1010 1015 1020
 Leu Tyr Ile Asp Ser Ile Arg Gln Tyr
 1025 1030

<210> 60

<211> 3352

<212> DNA

<213> Homo sapiens

<400> 60

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ctggagaagc ccttgccccc cagcatgggt ttctgccgca gcgcctgca cccgctgtct 180

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<210> 61

<211> 3257

<212> DNA

<213> Homo sapiens

<400> 61

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 cgtggtgctg gtgacccga gccctgacgg ccgcccctcc cgctacgtgc ggctgcgcca 3060
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<210> 62

<211> 1032

<212> PRT

<213> Homo sapiens

<400> 62

Met Gly Phe Cys Arg Ser Ala Leu His Pro Leu Ser Leu Leu Val Gln
 1 5 10 15
 Ala Ile Met Leu Ala Met Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
 20 25 30
 Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
 35 40 45
 Phe Leu Lys Ser Val Pro His Phe Ser Met Ala Ala Pro Arg Gly Asn
 50 55 60
 Val Thr Ser Leu Ser Leu Ser Ser Asn Arg Ile His His Leu His Asp
 65 70 75 80
 Ser Asp Phe Ala His Leu Pro Ser Leu Arg His Leu Asn Leu Lys Trp
 85 90 95
 Asn Cys Pro Pro Val Gly Leu Ser Pro Met His Phe Pro Cys His Met

[illegible]

		435					440					445			
Gln	Pro	Gly	Asp	Leu	Ala	Pro	Ala	Pro	Val	Asp	Thr	Pro	Ser	Ser	Glu
	450					455					460				
Asp	Phe	Arg	Pro	Asn	Cys	Ser	Thr	Leu	Asn	Phe	Thr	Leu	Asp	Leu	Ser
465					470					475					480
Arg	Asn	Asn	Leu	Val	Thr	Val	Gln	Pro	Glu	Met	Phe	Ala	Gln	Leu	Ser
				485					490					495	
His	Leu	Gln	Cys	Leu	Arg	Leu	Ser	His	Asn	Cys	Ile	Ser	Gln	Ala	Val
			500					505					510		
Asn	Gly	Ser	Gln	Phe	Leu	Pro	Leu	Thr	Gly	Leu	Gln	Val	Leu	Asp	Leu
		515					520					525			
Ser	Arg	Asn	Lys	Leu	Asp	Leu	Tyr	His	Glu	His	Ser	Phe	Thr	Glu	Leu
	530					535					540				
Pro	Arg	Leu	Glu	Ala	Leu	Asp	Leu	Ser	Tyr	Asn	Ser	Gln	Pro	Phe	Gly
545					550					555					560
Met	Gln	Gly	Val	Gly	His	Asn	Phe	Ser	Phe	Val	Ala	His	Leu	Arg	Thr
				565					570					575	
Leu	Arg	His	Leu	Ser	Leu	Ala	His	Asn	Asn	Ile	His	Ser	Gln	Val	Ser
			580					585					590		
Gln	Gln	Leu	Cys	Ser	Thr	Ser	Leu	Arg	Ala	Leu	Asp	Phe	Ser	Gly	Asn
		595					600					605			
Ala	Leu	Gly	His	Met	Trp	Ala	Glu	Gly	Asp	Leu	Tyr	Leu	His	Phe	Phe
	610					615					620				
Gln	Gly	Leu	Ser	Gly	Leu	Ile	Trp	Leu	Asp	Leu	Ser	Gln	Asn	Arg	Leu
625					630					635					640
His	Thr	Leu	Leu	Pro	Gln	Thr	Leu	Arg	Asn	Leu	Pro	Lys	Ser	Leu	Gln
				645					650					655	
Val	Leu	Arg	Leu	Arg	Asp	Asn	Tyr	Leu	Ala	Phe	Phe	Lys	Trp	Trp	Ser
			660					665					670		
Leu	His	Phe	Leu	Pro	Lys	Leu	Glu	Val	Leu	Asp	Leu	Ala	Gly	Asn	Arg
		675					680					685			
Leu	Lys	Ala	Leu	Thr	Asn	Gly	Ser	Leu	Pro	Ala	Gly	Thr	Arg	Leu	Arg
	690					695					700				
Arg	Leu	Asp	Val	Ser	Cys	Asn	Ser	Ile	Ser	Phe	Val	Ala	Pro	Gly	Phe
705					710					715					720
Phe	Ser	Lys	Ala	Lys	Glu	Leu	Arg	Glu	Leu	Asn	Leu	Ser	Ala	Asn	Ala
				725					730					735	
Leu	Lys	Thr	Val	Asp	His	Ser	Trp	Phe	Gly	Pro	Leu	Ala	Ser	Ala	Leu
			740					745					750		
Gln	Ile	Leu	Asp	Val	Ser	Ala	Asn	Pro	Leu	His	Cys	Ala	Cys	Gly	Ala
		755					760					765			
Ala	Phe	Met	Asp	Phe	Leu	Leu	Glu	Val	Gln	Ala	Ala	Val	Pro	Gly	Leu

770	775	780
Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Leu Ser		
785	790	795 800
Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp		
	805	810 815
Asp Cys Phe Ala Leu Ser Leu Leu Ala Val Ala Leu Gly Leu Gly Val		
	820	825 830
Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His		
	835	840 845
Leu Cys Leu Ala Trp Leu Pro Trp Arg Gly Arg Gln Ser Gly Arg Asp		
	850	855 860
Glu Asp Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Thr Gln		
	865	870 875 880
Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Gly Gln Leu Glu		
	885	890 895
Glu Cys Arg Gly Arg Trp Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp		
	900	905 910
Trp Leu Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr		
	915	920 925
Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser		
	930	935 940
Gly Leu Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu		
	945	950 955 960
Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Ser Pro Asp Gly Arg		
	965	970 975
Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val		
	980	985 990
Leu Leu Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln		
	995	1000 1005
Leu Gly Met Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg		
	1010	1015 1020
Asn Phe Cys Gln Gly Pro Thr Ala Glu		
	1025	1030

<210> 63
 <211> 1032
 <212> PRT
 <213> Homo sapiens

<400> 63

Met Gly Phe Cys Arg Ser Ala Leu His Pro Leu Ser Leu Leu Val Gln		
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Ala Ile Met Leu Ala Met Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe		
	20	25 30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
 35 40 45
 Phe Leu Lys Ser Val Pro His Phe Ser Met Ala Ala Pro Arg Gly Asn
 50 55 60
 Val Thr Ser Leu Ser Leu Ser Ser Asn Arg Ile His His Leu His Asp
 65 70 75 80
 Ser Asp Phe Ala His Leu Pro Ser Leu Arg His Leu Asn Leu Lys Trp
 85 90 95
 Asn Cys Pro Pro Val Gly Leu Ser Pro Met His Phe Pro Cys His Met
 100 105 110
 Thr Ile Glu Pro Ser Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
 115 120 125
 Asn Leu Ser Tyr Asn Asn Ile Met Thr Val Pro Ala Leu Pro Lys Ser
 130 135 140
 Leu Ile Ser Leu Ser Leu Ser His Thr Asn Ile Leu Met Leu Asp Ser
 145 150 155 160
 Ala Ser Leu Ala Gly Leu His Ala Leu Arg Phe Leu Phe Met Asp Gly
 165 170 175
 Asn Cys Tyr Tyr Lys Asn Pro Cys Arg Gln Ala Leu Glu Val Ala Pro
 180 185 190
 Gly Ala Leu Leu Gly Leu Gly Asn Leu Thr His Leu Ser Leu Lys Tyr
 195 200 205
 Asn Asn Leu Thr Val Val Pro Arg Asn Leu Pro Ser Ser Leu Glu Tyr
 210 215 220
 Leu Leu Leu Ser Tyr Asn Arg Ile Val Lys Leu Ala Pro Glu Asp Leu
 225 230 235 240
 Ala Asn Leu Thr Ala Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
 245 250 255
 Arg Cys Asp His Ala Pro Asn Pro Cys Met Glu Cys Pro Arg His Phe
 260 265 270
 Pro Gln Leu His Pro Asp Thr Phe Ser His Leu Ser Arg Leu Glu Gly
 275 280 285
 Leu Val Leu Lys Asp Ser Ser Leu Ser Trp Leu Asn Ala Ser Trp Phe
 290 295 300
 Arg Gly Leu Gly Asn Leu Arg Val Leu Asp Leu Ser Glu Asn Phe Leu
 305 310 315 320
 Tyr Lys Cys Ile Thr Lys Thr Lys Ala Phe Gln Gly Leu Thr Gln Leu
 325 330 335
 Arg Lys Leu Asn Leu Ser Phe Asn Tyr Gln Lys Arg Val Ser Phe Ala
 340 345 350
 His Leu Ser Leu Ala Pro Ser Phe Gly Ser Leu Val Ala Leu Lys Glu

355	360	365																	
Leu	Asp	Met	His	Gly	Ile	Phe	Phe	Arg	Ser	Leu	Asp	Glu	Thr	Thr	Leu				
370						375					380								
Arg	Pro	Leu	Ala	Arg	Leu	Pro	Met	Leu	Gln	Thr	Leu	Arg	Leu	Gln	Met				
385					390					395					400				
Asn	Phe	Ile	Asn	Gln	Ala	Gln	Leu	Gly	Ile	Phe	Arg	Ala	Phe	Pro	Gly				
				405					410					415					
Leu	Arg	Tyr	Val	Asp	Leu	Ser	Asp	Asn	Arg	Ile	Ser	Gly	Ala	Ser	Glu				
			420					425					430						
Leu	Thr	Ala	Thr	Met	Gly	Glu	Ala	Asp	Gly	Gly	Glu	Lys	Val	Trp	Leu				
		435					440					445							
Gln	Pro	Gly	Asp	Leu	Ala	Pro	Ala	Pro	Val	Asp	Thr	Pro	Ser	Ser	Glu				
450						455					460								
Asp	Phe	Arg	Pro	Asn	Cys	Ser	Thr	Leu	Asn	Phe	Thr	Leu	Asp	Leu	Ser				
465					470					475					480				
Arg	Asn	Asn	Leu	Val	Thr	Val	Gln	Pro	Glu	Met	Phe	Ala	Gln	Leu	Ser				
				485					490					495					
His	Leu	Gln	Cys	Leu	Arg	Leu	Ser	His	Asn	Cys	Ile	Ser	Gln	Ala	Val				
			500					505					510						
Asn	Gly	Ser	Gln	Phe	Leu	Pro	Leu	Thr	Gly	Leu	Gln	Val	Leu	Asp	Leu				
		515					520					525							
Ser	His	Asn	Lys	Leu	Asp	Leu	Tyr	His	Glu	His	Ser	Phe	Thr	Glu	Leu				
530						535					540								
Pro	Arg	Leu	Glu	Ala	Leu	Asp	Leu	Ser	Tyr	Asn	Ser	Gln	Pro	Phe	Gly				
545					550					555					560				
Met	Gln	Gly	Val	Gly	His	Asn	Phe	Ser	Phe	Val	Ala	His	Leu	Arg	Thr				
				565					570					575					
Leu	Arg	His	Leu	Ser	Leu	Ala	His	Asn	Asn	Ile	His	Ser	Gln	Val	Ser				
			580					585					590						
Gln	Gln	Leu	Cys	Ser	Thr	Ser	Leu	Arg	Ala	Leu	Asp	Phe	Ser	Gly	Asn				
		595					600					605							
Ala	Leu	Gly	His	Met	Trp	Ala	Glu	Gly	Asp	Leu	Tyr	Leu	His	Phe	Phe				
610						615					620								
Gln	Gly	Leu	Ser	Gly	Leu	Ile	Trp	Leu	Asp	Leu	Ser	Gln	Asn	Arg	Leu				
625					630					635					640				
His	Thr	Leu	Leu	Pro	Gln	Thr	Leu	Arg	Asn	Leu	Pro	Lys	Ser	Leu	Gln				
				645					650					655					
Val	Leu	Arg	Leu	Arg	Asp	Asn	Tyr	Leu	Ala	Phe	Phe	Lys	Trp	Trp	Ser				
			660					665					670						
Leu	His	Phe	Leu	Pro	Lys	Leu	Glu	Val	Leu	Asp	Leu	Ala	Gly	Asn	Gln				
		675					680					685							
Leu	Lys	Ala	Leu	Thr	Asn	Gly	Ser	Leu	Pro	Ala	Gly	Thr	Arg	Leu	Arg				

690	695	700
Arg Leu Asp Val Ser Cys Asn Ser Ile Ser Phe Val Ala Pro Gly Phe		
705	710	715 720
Phe Ser Lys Ala Lys Glu Leu Arg Glu Leu Asn Leu Ser Ala Asn Ala		
	725	730 735
Leu Lys Thr Val Asp His Ser Trp Phe Gly Pro Leu Ala Ser Ala Leu		
	740	745 750
Gln Ile Leu Asp Val Ser Ala Asn Pro Leu His Cys Ala Cys Gly Ala		
	755	760 765
Ala Phe Met Asp Phe Leu Leu Glu Val Gln Ala Ala Val Pro Gly Leu		
	770	775 780
Pro Ser Arg Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Leu Ser		
	785	790 795 800
Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Ala Leu Ser Trp		
	805	810 815
Asp Cys Phe Ala Leu Ser Leu Leu Ala Val Ala Leu Gly Leu Gly Val		
	820	825 830
Pro Met Leu His His Leu Cys Gly Trp Asp Leu Trp Tyr Cys Phe His		
	835	840 845
Leu Cys Leu Ala Trp Leu Pro Trp Arg Gly Arg Gln Ser Gly Arg Asp		
	850	855 860
Glu Asp Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Thr Gln		
	865	870 875 880
Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Gly Gln Leu Glu		
	885	890 895
Glu Cys Arg Gly Arg Trp Ala Leu Arg Leu Cys Leu Glu Glu Arg Asp		
	900	905 910
Trp Leu Pro Gly Lys Thr Leu Phe Glu Asn Leu Trp Ala Ser Val Tyr		
	915	920 925
Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser		
	930	935 940
Gly Leu Leu Arg Ala Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu		
	945	950 955 960
Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Ser Pro Asp Gly Arg		
	965	970 975
Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val		
	980	985 990
Leu Leu Trp Pro His Gln Pro Ser Gly Gln Arg Ser Phe Trp Ala Gln		
	995	1000 1005
Leu Gly Met Ala Leu Thr Arg Asp Asn His His Phe Tyr Asn Arg		
	1010	1015 1020
Asn Phe Cys Gln Gly Pro Thr Ala Glu		

1025 1030

<210> 64
 <211> 333
 <212> PRT
 <213> Homo sapiens

<400> 64

Met Pro Met Lys Trp Ser Gly Trp Arg Trp Ser Trp Gly Pro Ala Thr
 1 5 10 15

His Thr Ala Leu Pro Pro Pro Gln Gly Phe Cys Arg Ser Ala Leu His
 20 25 30

Pro Leu Ser Leu Leu Val Gln Ala Ile Met Leu Ala Met Thr Leu Ala
 35 40 45

Leu Gly Thr Leu Pro Ala Phe Leu Pro Cys Glu Leu Gln Pro His Gly
 50 55 60

Leu Val Asn Cys Asn Trp Leu Phe Leu Lys Ser Val Pro His Phe Ser
 65 70 75 80

Met Ala Ala Pro Arg Gly Asn Val Thr Ser Leu Ser Leu Ser Ser Asn
 85 90 95

Arg Ile His His Leu His Asp Ser Asp Phe Ala His Leu Pro Ser Leu
 100 105 110

Arg His Leu Asn Leu Lys Trp Asn Cys Pro Pro Val Gly Leu Ser Pro
 115 120 125

Met His Phe Pro Cys His Met Thr Ile Glu Pro Ser Thr Phe Leu Ala
 130 135 140

Val Pro Thr Leu Glu Glu Leu Asn Leu Ser Tyr Asn Asn Ile Met Thr
 145 150 155 160

Val Pro Ala Leu Pro Lys Ser Leu Ile Ser Leu Ser Leu Ser His Thr
 165 170 175

Asn Ile Leu Met Leu Asp Ser Ala Ser Leu Ala Gly Leu His Ala Leu
 180 185 190

Arg Phe Leu Phe Met Asp Gly Asn Cys Tyr Tyr Lys Asn Pro Cys Arg
 195 200 205

Gln Ala Leu Glu Val Ala Pro Gly Ala Leu Leu Gly Leu Gly Asn Leu
 210 215 220

Thr His Leu Ser Leu Lys Tyr Asn Asn Leu Thr Val Val Pro Arg Asn
 225 230 235 240

Leu Pro Ser Ser Leu Glu Tyr Leu Leu Leu Ser Tyr Asn Arg Ile Val
 245 250 255

Lys Leu Ala Pro Glu Asp Leu Ala Asn Leu Thr Ala Leu Arg Val Leu
 260 265 270

Asp Val Gly Gly Asn Cys Arg Arg Cys Asp His Ala Pro Asn Pro Cys
 275 280 285

Met Glu Cys Pro Arg His Phe Pro Gln Leu His Pro Asp Thr Phe Ser
 290 295 300
 His Leu Ser Arg Leu Glu Gly Leu Val Leu Lys Asp Ser Ser Leu Ser
 305 310 315 320
 Trp Leu Asn Ala Ser Trp Phe Arg Gly Leu Gly Asn Leu
 325 330

<210> 65
 <211> 216
 <212> PRT
 <213> Homo sapiens

<400> 65

Met Leu Tyr Ser Ser Cys Lys Ser Arg Leu Leu Asp Ser Val Glu Gln
 1 5 10 15
 Asp Phe His Leu Glu Ile Ala Lys Lys Gly Phe Cys Arg Ser Ala Leu
 20 25 30
 His Pro Leu Ser Leu Leu Val Gln Ala Ile Met Leu Ala Met Thr Leu
 35 40 45
 Ala Leu Gly Thr Leu Pro Ala Phe Leu Pro Cys Glu Leu Gln Pro His
 50 55 60
 Gly Leu Val Asn Cys Asn Trp Leu Phe Leu Lys Ser Val Pro His Phe
 65 70 75 80
 Ser Met Ala Ala Pro Arg Gly Asn Val Thr Ser Leu Ser Leu Ser Ser
 85 90 95
 Asn Arg Ile His His Leu His Asp Ser Asp Phe Ala His Leu Pro Ser
 100 105 110
 Leu Arg His Leu Asn Leu Lys Trp Asn Cys Pro Pro Val Gly Leu Ser
 115 120 125
 Pro Met His Phe Pro Cys His Met Thr Ile Glu Pro Ser Thr Phe Leu
 130 135 140
 Ala Val Pro Thr Leu Glu Glu Leu Asn Leu Ser Tyr Asn Asn Ile Met
 145 150 155 160
 Thr Val Pro Ala Leu Pro Lys Ser Leu Ile Ser Leu Ser Leu Ser His
 165 170 175
 Thr Asn Ile Leu Met Leu Asp Ser Ala Ser Leu Ala Gly Leu His Ala
 180 185 190
 Leu Arg Phe Leu Phe Met Asp Gly Asn Cys Tyr Tyr Lys Asn Pro Cys
 195 200 205
 Arg Gln Ala Leu Glu Val Ala Pro
 210 215

<210> 66

<211> 117
 <212> PRT
 <213> Homo sapiens

<400> 66

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Met Ala Ile Met Leu Ala Met Thr Leu Ala Leu Gly Thr Leu Pro Ala
1          5          10          15

Phe Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp
          20          25          30

Leu Phe Leu Lys Ser Val Pro His Phe Ser Met Ala Ala Pro Arg Gly
          35          40          45

Asn Val Thr Ser Leu Ser Leu Ser Ser Asn Arg Ile His His Leu His
          50          55          60

Asp Ser Asp Phe Ala His Leu Pro Ser Leu Arg His Leu Asn Leu Lys
65          70          75          80

Trp Asn Cys Pro Pro Val Gly Leu Ser Pro Met His Phe Pro Cys His
          85          90          95

Met Thr Ile Glu Pro Ser Thr Phe Leu Ala Val Pro Thr Leu Glu Glu
          100          105          110

Leu Asn Leu Ser Tyr
          115

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<210> 67
 <211> 1032
 <212> PRT
 <213> Homo sapiens

<400> 67

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Met Gly Phe Cys Arg Ser Ala Leu His Pro Leu Ser Leu Leu Val Gln
1          5          10          15

Ala Ile Met Leu Ala Met Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
          20          25          30

Leu Pro Cys Glu Leu Gln Pro His Gly Leu Val Asn Cys Asn Trp Leu
          35          40          45

Phe Leu Lys Ser Val Pro His Phe Ser Met Ala Ala Pro Arg Gly Asn
          50          55          60

Val Thr Ser Leu Ser Leu Ser Ser Asn Arg Ile His His Leu His Asp
65          70          75          80

Ser Asp Phe Ala His Leu Pro Ser Leu Arg His Leu Asn Leu Lys Trp
          85          90          95

Asn Cys Pro Pro Val Gly Leu Ser Pro Met His Phe Pro Cys His Met
          100          105          110

Thr Ile Glu Pro Ser Thr Phe Leu Ala Val Pro Thr Leu Glu Glu Leu
          115          120          125

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Asn	Leu	Ser	Tyr	Asn	Asn	Ile	Met	Thr	Val	Pro	Ala	Leu	Pro	Lys	Ser	130	135	140
Leu	Ile	Ser	Leu	Ser	Leu	Ser	His	Thr	Asn	Ile	Leu	Met	Leu	Asp	Ser	145	150	155
Ala	Ser	Leu	Ala	Gly	Leu	His	Ala	Leu	Arg	Phe	Leu	Phe	Met	Asp	Gly	165	170	175
Asn	Cys	Tyr	Tyr	Lys	Asn	Pro	Cys	Arg	Gln	Ala	Leu	Glu	Val	Ala	Pro	180	185	190
Gly	Ala	Leu	Leu	Gly	Leu	Gly	Asn	Leu	Thr	His	Leu	Ser	Leu	Lys	Tyr	195	200	205
Asn	Asn	Leu	Thr	Val	Val	Pro	Arg	Asn	Leu	Pro	Ser	Ser	Leu	Glu	Tyr	210	215	220
Leu	Leu	Leu	Ser	Tyr	Asn	Arg	Ile	Val	Lys	Leu	Ala	Pro	Glu	Asp	Leu	225	230	235
Ala	Asn	Leu	Thr	Ala	Leu	Arg	Val	Leu	Asp	Val	Gly	Gly	Asn	Cys	Arg	245	250	255
Arg	Cys	Asp	His	Ala	Pro	Asn	Pro	Cys	Met	Glu	Cys	Pro	Arg	His	Phe	260	265	270
Pro	Gln	Leu	His	Pro	Asp	Thr	Phe	Ser	His	Leu	Ser	Arg	Leu	Glu	Gly	275	280	285
Leu	Val	Leu	Lys	Asp	Ser	Ser	Leu	Ser	Trp	Leu	Asn	Ala	Ser	Trp	Phe	290	295	300
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Tyr	Lys	Cys	Ile	Thr	Lys	Thr	Lys	Ala	Phe	Gln	Gly	Leu	Thr	Gln	Leu	325	330	335
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His	Leu	Ser	Leu	Ala	Pro	Ser	Phe	Gly	Ser	Leu	Val	Ala	Leu	Lys	Glu	355	360	365
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Arg	Pro	Leu	Ala	Arg	Leu	Pro	Met	Leu	Gln	Thr	Leu	Arg	Leu	Gln	Met	385	390	395
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ccaaccgtat	ccaccacctg
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<210> 72
 <211> 1032
 <212> PRT
 <213> murine

<400> 72

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Met Val Leu Arg Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln
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Ala Ala Val Leu Ala Glu Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
20           25           30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu
35           40           45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Ser Cys Ser Asn
50           55           60

Ile Thr Arg Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asn
65           70           75           80

Ser Asp Phe Val His Leu Ser Asn Leu Arg Gln Leu Asn Leu Lys Trp
85           90           95

Asn Cys Pro Pro Thr Gly Leu Ser Pro Leu His Phe Ser Cys His Met
100          105          110

Thr Ile Glu Pro Arg Thr Phe Leu Ala Met Arg Thr Leu Glu Glu Leu
115          120          125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser
130          135          140

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Leu Val Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala
 145 150 155 160
 Asn Ser Leu Ala Gly Leu Tyr Ser Leu Arg Val Leu Phe Met Asp Gly
 165 170 175
 Asn Cys Tyr Tyr Lys Asn Pro Cys Thr Gly Ala Val Lys Val Thr Pro
 180 185 190
 Gly Ala Leu Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr
 195 200 205
 Asn Asn Leu Thr Lys Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr
 210 215 220
 Leu Leu Val Ser Tyr Asn Leu Ile Val Lys Leu Gly Pro Glu Asp Leu
 225 230 235 240
 Ala Asn Leu Thr Ser Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
 245 250 255
 Arg Cys Asp His Ala Pro Asn Pro Cys Ile Glu Cys Gly Gln Lys Ser
 260 265 270
 Leu His Leu His Pro Glu Thr Phe His His Leu Ser His Leu Glu Gly
 275 280 285
 Leu Val Leu Lys Asp Ser Ser Leu His Thr Leu Asn Ser Ser Trp Phe
 290 295 300
 Gln Gly Leu Val Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu
 305 310 315 320
 Tyr Glu Ser Ile Asn His Thr Asn Ala Phe Gln Asn Leu Thr Arg Leu
 325 330 335
 Arg Lys Leu Asn Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala
 340 345 350
 Arg Leu His Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu
 355 360 365
 Leu Asn Met Asn Gly Ile Phe Phe Arg Ser Leu Asn Lys Tyr Thr Leu
 370 375 380
 Arg Trp Leu Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met
 385 390 395 400
 Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala
 405 410 415
 Leu Arg Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr
 420 425 430
 Leu Ser Glu Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu
 435 440 445
 Leu Leu Ser Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser
 450 455 460
 Lys Asn Phe Met Asp Arg Cys Lys Asn Phe Lys Phe Thr Met Asp Leu

465 470 475 480
 Ser Arg Asn Asn Leu Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu
 485 490 495

 Ser Arg Leu Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala
 500 505 510

 Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Gln Val Leu Asp
 515 520 525

 Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys Ser Phe Ser Glu
 530 535 540

 Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe
 545 550 555 560

 Ser Met Lys Gly Ile Gly His Asn Phe Ser Phe Val Ala His Leu Ser
 565 570 575

 Met Leu His Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val
 580 585 590

 Ser Ser His Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly
 595 600 605

 Asn Gly Met Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe
 610 615 620

 Phe Gln Gly Leu Ser Gly Leu Leu Lys Leu Asp Leu Ser Gln Asn Asn
 625 630 635 640

 Leu His Ile Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu
 645 650 655

 Lys Leu Leu Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr
 660 665 670

 Ser Leu Ser Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn
 675 680 685

 Gln Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu
 690 695 700

 Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Ser Val Val Pro Ala
 705 710 715 720

 Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn
 725 730 735

 Ile Leu Lys Thr Val Asp Arg Ser Trp Phe Gly Pro Ile Val Met Asn
 740 745 750

 Leu Thr Val Leu Asp Val Arg Ser Asn Pro Leu His Cys Ala Cys Gly
 755 760 765

 Ala Ala Phe Val Asp Leu Leu Leu Glu Val Gln Thr Lys Val Pro Gly
 770 775 780

 Leu Ala Asn Gly Val Lys Cys Gly Ser Pro Gly Gln Leu Gln Gly Arg
 785 790 795 800

 Ser Ile Phe Ala Gln Asp Leu Arg Leu Cys Leu Asp Glu Val Leu Ser

805 810 815
 Trp Asp Cys Phe Gly Leu Ser Leu Leu Ala Val Ala Val Gly Met Val
 820 825 830
 Val Pro Ile Leu His His Leu Cys Gly Trp Asp Val Trp Tyr Cys Phe
 835 840 845
 His Leu Cys Leu Ala Trp Leu Pro Leu Leu Ala Arg Ser Arg Arg Ser
 850 855 860
 Ala Gln Ala Leu Pro Tyr Asp Ala Phe Val Val Phe Asp Lys Ala Gln
 865 870 875 880
 Ser Ala Val Ala Asp Trp Val Tyr Asn Glu Leu Arg Val Arg Leu Glu
 885 890 895
 Glu Arg Arg Gly Arg Arg Ala Leu Arg Leu Cys Leu Glu Asp Arg Asp
 900 905 910
 Trp Leu Pro Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr
 915 920 925
 Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser
 930 935 940
 Gly Leu Leu Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu
 945 950 955 960
 Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His
 965 970 975
 Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val
 980 985 990
 Leu Phe Trp Pro Gln Gln Pro Asn Gly Gln Gly Gly Phe Trp Ala Gln
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 Asn Phe Cys Arg Gly Pro Thr Ala Glu
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<210> 73
 <211> 1032
 <212> PRT
 <213> murine

<400> 73

Met Val Leu Arg Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln
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 Ala Ala Val Leu Ala Glu Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
 20 25 30
 Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu
 35 40 45
 Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Ser Cys Ser Asn
 50 55 60

Ile Thr Arg Leu Ser	Leu Ile Ser Asn Arg	Ile His His Leu His Asn	65	70	75	80
Ser Asp Phe Val His	Leu Ser Asn Leu Arg	Gln Leu Asn Leu Lys Trp	85	90	95	
Asn Cys Pro Pro Thr	Gly Leu Ser Pro Leu	His Phe Ser Cys His Met	100	105	110	
Thr Ile Glu Pro Arg	Thr Phe Leu Ala Met	Arg Thr Leu Glu Glu Leu	115	120	125	
Asn Leu Ser Tyr Asn	Gly Ile Thr Thr Val	Pro Arg Leu Pro Ser Ser	130	135	140	
Leu Val Asn Leu Ser	Leu Ser His Thr Asn	Ile Leu Val Leu Asp Ala	145	150	155	160
Asn Ser Leu Ala Gly	Leu Tyr Ser Leu Arg	Val Leu Phe Met Asp Gly	165	170	175	
Asn Cys Tyr Tyr Lys	Asn Pro Cys Thr Gly	Ala Val Lys Val Thr Pro	180	185	190	
Gly Ala Leu Leu Gly	Leu Ser Asn Leu Thr	His Leu Ser Leu Lys Tyr	195	200	205	
Asn Asn Leu Thr Lys	Val Pro Arg Gln Leu	Pro Pro Ser Leu Glu Tyr	210	215	220	
Leu Leu Val Ser Tyr	Asn Leu Ile Val Lys	Leu Gly Pro Glu Asp Leu	225	230	235	240
Ala Asn Leu Thr Ser	Leu Arg Val Leu Asp	Val Gly Gly Asn Cys Arg	245	250	255	
Arg Cys Asp His Ala	Pro Asn Pro Cys Ile	Glu Cys Gly Gln Lys Ser	260	265	270	
Leu His Leu His Pro	Glu Thr Phe His His	Leu Ser His Leu Glu Gly	275	280	285	
Leu Val Leu Lys Asp	Ser Ser Leu His Thr	Leu Asn Ser Ser Trp Phe	290	295	300	
Gln Gly Leu Val Asn	Leu Ser Val Leu Asp	Leu Ser Glu Asn Phe Leu	305	310	315	320
Tyr Glu Ser Ile Asn	His Thr Asn Ala Phe	Gln Asn Leu Thr Arg Leu	325	330	335	
Arg Lys Leu Asn Leu	Ser Phe Asn Tyr Arg	Lys Lys Val Ser Phe Ala	340	345	350	
Arg Leu His Leu Ala	Ser Ser Phe Lys Asn	Leu Val Ser Leu Gln Glu	355	360	365	
Leu Asn Met Asn Gly	Ile Phe Phe Arg Ser	Leu Asn Lys Tyr Thr Leu	370	375	380	
Arg Trp Leu Ala Asp	Leu Pro Lys Leu His	Thr Leu His Leu Gln Met				

385	390	395	400
Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala			
405	410	415	
Leu Arg Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr			
420	425	430	
Leu Ser Glu Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu			
435	440	445	
Leu Leu Ser Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser			
450	455	460	
Lys Asn Phe Met Asp Arg Cys Lys Asn Phe Lys Phe Thr Met Asp Leu			
465	470	475	480
Ser Arg Asn Asn Leu Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu			
485	490	495	
Ser Arg Leu Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala			
500	505	510	
Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Gln Val Leu Asp			
515	520	525	
Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys Ser Phe Ser Glu			
530	535	540	
Leu Pro Gln Leu Gln Ala Leu Asp Leu Gly Tyr Asn Ser Gln Pro Phe			
545	550	555	560
Ser Ile Lys Gly Ile Gly His Asn Phe Ser Phe Val Ala His Leu Ser			
565	570	575	
Met Leu His Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val			
580	585	590	
Ser Ser His Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly			
595	600	605	
Asn Gly Met Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe			
610	615	620	
Phe Gln Gly Leu Ser Gly Leu Leu Lys Leu Asp Leu Ser Gln Asn Asn			
625	630	635	640
Leu His Ile Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu			
645	650	655	
Lys Leu Leu Ser Leu Arg Asp Asn Tyr Leu Ser Phe Phe Asn Trp Thr			
660	665	670	
Ser Leu Ser Phe Leu Pro Asn Leu Glu Val Leu Asp Leu Ala Gly Asn			
675	680	685	
Gln Leu Lys Ala Leu Thr Asn Gly Thr Leu Pro Asn Gly Thr Leu Leu			
690	695	700	
Gln Lys Leu Asp Val Ser Ser Asn Ser Ile Val Ser Val Val Pro Ala			
705	710	715	720
Phe Phe Ala Leu Ala Val Glu Leu Lys Glu Val Asn Leu Ser His Asn			

Ile	Leu	Lys	Thr	Val	Asp	Arg	Ser	Trp	Phe	Gly	Pro	Ile	Val	Met	Asn
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				740					745					750	
Leu	Thr	Val	Leu	Asp	Val	Arg	Ser	Asn	Pro	Leu	His	Cys	Ala	Cys	Gly
				755				760					765		
Ala	Ala	Phe	Val	Asp	Leu	Leu	Leu	Glu	Val	Gln	Thr	Lys	Val	Pro	Gly
				770				775				780			
Leu	Ala	Asn	Gly	Val	Lys	Cys	Gly	Ser	Pro	Gly	Gln	Leu	Gln	Gly	Arg
				785				790				795			800
Ser	Ile	Phe	Ala	Gln	Asp	Leu	Arg	Leu	Cys	Leu	Asp	Glu	Val	Leu	Ser
				805					810					815	
Trp	Asp	Cys	Phe	Gly	Leu	Ser	Leu	Leu	Ala	Val	Ala	Val	Gly	Met	Val
				820					825					830	
Val	Pro	Ile	Leu	His	His	Leu	Cys	Gly	Trp	Asp	Val	Trp	Tyr	Cys	Phe
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His	Leu	Cys	Leu	Ala	Trp	Leu	Pro	Leu	Leu	Ala	Arg	Ser	Arg	Arg	Ser
				850					855					860	
Ala	Gln	Ala	Leu	Pro	Tyr	Asp	Ala	Phe	Val	Val	Phe	Asp	Lys	Ala	Gln
				865					870					875	880
Ser	Ala	Val	Ala	Asp	Trp	Val	Tyr	Asn	Glu	Leu	Arg	Val	Arg	Leu	Glu
				885					890					895	
Gly	Arg	Arg	Gly	Arg	Arg	Ala	Leu	Arg	Leu	Cys	Leu	Glu	Asp	Arg	Asp
				900					905					910	
Trp	Leu	Pro	Gly	Gln	Thr	Leu	Phe	Glu	Asn	Leu	Trp	Ala	Ser	Ile	Tyr
				915					920					925	
Gly	Ser	Arg	Lys	Thr	Leu	Phe	Val	Leu	Ala	His	Thr	Asp	Arg	Val	Ser
				930					935					940	
Gly	Leu	Leu	Arg	Thr	Ser	Phe	Leu	Leu	Ala	Gln	Gln	Arg	Leu	Leu	Glu
				945					950					955	960
Asp	Arg	Lys	Asp	Val	Val	Val	Leu	Val	Ile	Leu	Arg	Pro	Asp	Ala	His
				965					970					975	
Arg	Ser	Arg	Tyr	Val	Arg	Leu	Arg	Gln	Arg	Leu	Cys	Arg	Gln	Ser	Val
				980					985					990	
Leu	Phe	Trp	Pro	Gln	Gln	Pro	Asn	Gly	Gln	Gly	Gly	Phe	Trp	Ala	Gln
				995					1000					1005	
Leu	Ser	Thr	Ala	Leu	Thr	Arg	Asp	Asn	Arg	His	Phe	Tyr	Asn	Gln	
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Asn	Phe	Cys	Arg	Gly	Pro	Thr	Ala	Glu							
				1025					1030						

<210> 74
 <211> 1032
 <212> PRT

<213> murine

<400> 74

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Met Val Leu Arg Arg Arg Thr Leu His Pro Leu Ser Leu Leu Val Gln
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Ala Ala Val Leu Ala Glu Thr Leu Ala Leu Gly Thr Leu Pro Ala Phe
20          25          30

Leu Pro Cys Glu Leu Lys Pro His Gly Leu Val Asp Cys Asn Trp Leu
35          40          45

Phe Leu Lys Ser Val Pro Arg Phe Ser Ala Ala Ala Ser Cys Ser Asn
50          55          60

Ile Thr Arg Leu Ser Leu Ile Ser Asn Arg Ile His His Leu His Asn
65          70          75          80

Ser Asp Phe Val His Leu Ser Asn Leu Arg Gln Leu Asn Leu Lys Trp
85          90          95

Asn Cys Pro Pro Thr Gly Leu Ser Pro Leu His Phe Ser Cys His Met
100         105         110

Thr Ile Glu Pro Arg Thr Phe Leu Ala Met Arg Thr Leu Glu Glu Leu
115         120         125

Asn Leu Ser Tyr Asn Gly Ile Thr Thr Val Pro Arg Leu Pro Ser Ser
130         135         140

Leu Val Asn Leu Ser Leu Ser His Thr Asn Ile Leu Val Leu Asp Ala
145         150         155         160

Asn Ser Leu Ala Gly Leu Tyr Ser Leu Arg Val Leu Phe Met Asp Gly
165         170         175

Asn Cys Tyr Tyr Lys Asn Pro Cys Thr Gly Ala Val Lys Val Thr Pro
180         185         190

Gly Ala Leu Leu Gly Leu Ser Asn Leu Thr His Leu Ser Leu Lys Tyr
195         200         205

Asn Asn Leu Thr Lys Val Pro Arg Gln Leu Pro Pro Ser Leu Glu Tyr
210         215         220

Leu Leu Val Ser Tyr Asn Leu Ile Val Lys Leu Gly Pro Glu Asp Leu
225         230         235         240

Ala Asn Leu Thr Ser Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
245         250         255

Arg Cys Asp His Ala Pro Asn Pro Cys Ile Glu Cys Gly Gln Lys Ser
260         265         270

Leu His Leu His Pro Glu Thr Phe His His Leu Ser His Leu Glu Gly
275         280         285

Leu Val Leu Lys Asp Ser Ser Leu His Thr Leu Asn Ser Ser Trp Phe
290         295         300

Gln Gly Leu Val Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu
305         310         315         320

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 Leu Asn Met Asn Gly Ile Phe Phe Arg Ser Leu Asn Lys Tyr Thr Leu
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 Arg Trp Leu Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met
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 Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala
 405 410 415
 Leu Arg Phe Val Asp Leu Ser Asp Asn Arg Ile Ser Gly Pro Ser Thr
 420 425 430
 Leu Ser Glu Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu
 435 440 445
 Leu Leu Ser Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser
 450 455 460
 Lys Asn Phe Met Asp Arg Cys Lys Asn Phe Lys Phe Thr Met Asp Leu
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 Ser Arg Asn Asn Leu Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu
 485 490 495
 Ser Arg Leu Gln Cys Leu Ser Leu Ser His Asn Ser Ile Ala Gln Ala
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 Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Gln Val Leu Asp
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 Leu Ser His Asn Lys Leu Asp Leu Tyr His Trp Lys Ser Phe Ser Glu
 530 535 540
 Leu Pro Gln Leu Gln Ala Leu Asp Leu Ser Tyr Asn Ser Gln Pro Phe
 545 550 555 560
 Ser Met Lys Gly Ile Gly His Asn Phe Ser Phe Val Thr His Leu Ser
 565 570 575
 Met Leu Gln Ser Leu Ser Leu Ala His Asn Asp Ile His Thr Arg Val
 580 585 590
 Ser Ser His Leu Asn Ser Asn Ser Val Arg Phe Leu Asp Phe Ser Gly
 595 600 605
 Asn Gly Met Gly Arg Met Trp Asp Glu Gly Gly Leu Tyr Leu His Phe
 610 615 620
 Phe Gln Gly Leu Ser Gly Leu Leu Lys Leu Asp Leu Ser Gln Asn Asn
 625 630 635 640
 Leu His Ile Leu Arg Pro Gln Asn Leu Asp Asn Leu Pro Lys Ser Leu

				645					650					655		
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Gln	Leu 690	Lys	Ala	Leu	Thr	Asn 695	Gly	Thr	Leu	Pro	Asn 700	Gly	Thr	Leu	Leu	
Gln 705	Lys	Leu	Asp	Val	Ser 710	Ser	Asn	Ser	Ile	Val 715	Ser	Val	Val	Pro	Ala 720	
Phe	Phe	Ala	Leu	Ala 725	Val	Glu	Leu	Lys	Glu 730	Val	Asn	Leu	Ser	His 735	Asn	
Ile	Leu	Lys	Thr 740	Val	Asp	Arg	Ser	Trp 745	Phe	Gly	Pro	Ile	Val 750	Met	Asn	
Leu	Thr	Val 755	Leu	Asp	Val	Arg	Ser 760	Asn	Pro	Leu	His	Cys 765	Ala	Cys	Gly	
Ala 770	Ala	Phe	Val	Asp	Leu	Leu 775	Leu	Glu	Val	Gln	Thr 780	Lys	Val	Pro	Gly	
Leu 785	Ala	Asn	Gly	Val	Lys 790	Cys	Gly	Ser	Pro	Gly 795	Gln	Leu	Gln	Gly	Arg 800	
Ser	Ile	Phe	Ala	Gln 805	Asp	Leu	Arg	Leu	Cys 810	Leu	Asp	Glu	Val	Leu 815	Ser	
Trp	Asp	Cys	Phe 820	Gly	Leu	Ser	Leu	Leu 825	Ala	Val	Ala	Val	Gly 830	Met	Val	
Val	Pro	Ile 835	Leu	His	His	Leu	Cys 840	Gly	Trp	Asp	Val	Trp 845	Tyr	Cys	Phe	
His 850	Leu	Cys	Leu	Ala	Trp 855	Leu	Pro	Leu	Leu	Ala	Arg 860	Ser	Arg	Arg	Ser	
Ala 865	Gln	Thr	Leu	Pro	Tyr 870	Asp	Ala	Phe	Val	Val 875	Phe	Asp	Lys	Ala	Gln 880	
Ser	Ala	Val	Ala	Asp 885	Trp	Val	Tyr	Asn	Glu 890	Leu	Arg	Val	Arg	Leu 895	Glu	
Glu	Arg	Arg 900	Gly	Arg	Arg	Ala	Leu 905	Arg	Leu	Cys	Leu	Glu 910	Asp	Arg	Asp	
Trp	Leu	Pro 915	Gly	Gln	Thr	Leu	Phe 920	Glu	Asn	Leu	Trp	Ala 925	Ser	Ile	Tyr	
Gly 930	Ser	Arg	Lys	Thr	Leu	Phe 935	Val	Leu	Ala	His	Thr 940	Asp	Arg	Val	Ser	
Gly 945	Leu	Leu	Arg	Thr	Ser 950	Phe	Leu	Leu	Ala	Gln 955	Gln	Arg	Leu	Leu	Glu 960	
Asp	Arg	Lys	Asp 965	Val	Val	Val	Leu	Val	Ile 970	Leu	Arg	Pro	Asp	Ala 975	His	
Arg	Ser	Arg	Tyr	Val	Arg	Leu	Arg	Gln	Arg	Leu	Cys	Arg	Gln	Ser	Val	

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          980                      985                      990
Leu Phe Trp Pro Gln Gln Pro Asn Gly Gln Gly Gly Phe Trp Ala Gln
      995                          1000 /                        1005


Leu Ser Thr Ala Leu Thr Arg Asp Asn Arg His Phe Tyr Asn Gln
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Asn Phe Cys Arg Gly Pro Thr Ala Glu
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Phe	Leu	Lys	Ser	Val	Pro	Arg	Phe	Ser	Ala	Ala	Ala	Ser	Cys	Ser	Asn
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Ser	Asp	Phe	Val	His	Leu	Ser	Asn	Leu	Arg	Gln	Leu	Asn	Leu	Lys	Trp
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Asn	Cys	Pro	Pro	Thr	Gly	Leu	Ser	Pro	Leu	His	Phe	Ser	Cys	His	Met
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Thr	Ile	Glu	Pro	Arg	Thr	Phe	Leu	Ala	Met	Arg	Thr	Leu	Glu	Glu	Leu
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Asn	Leu	Ser	Tyr	Asn	Gly	Ile	Thr	Thr	Val	Pro	Arg	Leu	Pro	Ser	Ser
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Leu	Val	Asn	Leu	Ser	Leu	Ser	His	Thr	Asn	Ile	Leu	Val	Leu	Asp	Ala
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Asn	Ser	Leu	Ala	Gly	Leu	Tyr	Ser	Leu	Arg	Val	Leu	Phe	Met	Asp	Gly
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Asn	Cys	Tyr	Tyr	Lys	Asn	Pro	Cys	Thr	Gly	Ala	Val	Lys	Val	Thr	Pro
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Gly	Ala	Leu	Leu	Gly	Leu	Ser	Asn	Leu	Thr	His	Leu	Ser	Leu	Lys	Tyr
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Asn	Asn	Leu	Thr	Lys	Val	Pro	Arg	Gln	Leu	Pro	Pro	Ser	Leu	Glu	Tyr
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Leu	Leu	Val	Ser	Tyr	Asn	Leu	Ile	Val	Lys	Leu	Gly	Pro	Glu	Asp	Leu
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Ala Asn Leu Thr Ser Leu Arg Val Leu Asp Val Gly Gly Asn Cys Arg
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 Arg Cys Asp His Ala Pro Asn Pro Cys Ile Glu Cys Gly Gln Lys Ser
 260 265 270
 Leu His Leu His Pro Glu Thr Phe His His Leu Ser His Leu Glu Gly
 275 280 285
 Leu Val Leu Lys Asp Ser Ser Leu His Thr Leu Asn Ser Ser Trp Phe
 290 295 300
 Gln Gly Leu Val Asn Leu Ser Val Leu Asp Leu Ser Glu Asn Phe Leu
 305 310 315 320
 Tyr Glu Ser Ile Asn His Thr Asn Ala Phe Gln Asn Leu Thr Arg Leu
 325 330 335
 Arg Lys Leu Asn Leu Ser Phe Asn Tyr Arg Lys Lys Val Ser Phe Ala
 340 345 350
 Arg Leu His Leu Ala Ser Ser Phe Lys Asn Leu Val Ser Leu Gln Glu
 355 360 365
 Leu Asn Met Asn Gly Ile Phe Phe Arg Ser Leu Asn Lys Tyr Thr Leu
 370 375 380
 Arg Trp Leu Ala Asp Leu Pro Lys Leu His Thr Leu His Leu Gln Met
 385 390 395 400
 Asn Phe Ile Asn Gln Ala Gln Leu Ser Ile Phe Gly Thr Phe Arg Ala
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 420 425 430
 Leu Ser Glu Ala Thr Pro Glu Glu Ala Asp Asp Ala Glu Gln Glu Glu
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 Leu Leu Ser Ala Asp Pro His Pro Ala Pro Leu Ser Thr Pro Ala Ser
 450 455 460
 Lys Asn Phe Met Asp Arg Cys Lys Asn Phe Lys Phe Thr Met Asp Leu
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 Ser Arg Asn Asn Leu Val Thr Ile Lys Pro Glu Met Phe Val Asn Leu
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 Val Asn Gly Ser Gln Phe Leu Pro Leu Thr Asn Leu Gln Val Leu Asp
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 545 550 555 560
 Ser Met Lys Gly Ile Gly His Asn Phe Ser Phe Val Thr His Leu Ser

				565					570					575			
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Ser	Ser	His	Leu	Asn	Ser	Asn	Ser	Val	Arg	Phe	Leu	Asp	Phe	Ser	Gly		
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Asn	Gly	Met	Gly	Arg	Met	Trp	Asp	Glu	Gly	Gly	Leu	Tyr	Leu	His	Phe		
	610					615					620						
Phe	Gln	Gly	Leu	Ser	Gly	Leu	Leu	Lys	Leu	Asp	Leu	Ser	Gln	Asn	Asn		
625					630					635					640		
Leu	His	Ile	Leu	Arg	Pro	Gln	Asn	Leu	Asp	Asn	Leu	Pro	Lys	Ser	Leu		
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Lys	Leu	Leu	Ser	Leu	Arg	Asp	Asn	Tyr	Leu	Ser	Phe	Phe	Asn	Trp	Thr		
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Ser	Leu	Ser	Phe	Leu	Pro	Asn	Leu	Glu	Val	Leu	Asp	Leu	Ala	Gly	Asn		
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Gln	Leu	Lys	Ala	Leu	Thr	Asn	Gly	Thr	Leu	Pro	Asn	Gly	Thr	Leu	Leu		
	690					695					700						
Gln	Lys	Leu	Asp	Val	Ser	Ser	Asn	Ser	Ile	Val	Ser	Val	Val	Pro	Ala		
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Phe	Phe	Ala	Leu	Ala	Val	Glu	Leu	Lys	Glu	Val	Asn	Leu	Ser	His	Asn		
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Ile	Leu	Lys	Thr	Val	Asp	Arg	Ser	Trp	Phe	Gly	Pro	Ile	Val	Met	Asn		
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Leu	Thr	Val	Leu	Asp	Val	Arg	Ser	Asn	Pro	Leu	His	Cys	Ala	Cys	Gly		
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Ala	Ala	Phe	Val	Asp	Leu	Leu	Leu	Glu	Val	Gln	Thr	Lys	Val	Pro	Gly		
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785					790					795					800		
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			805						810					815			
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			820					825						830			
Val	Pro	Ile	Leu	His	His	Leu	Cys	Gly	Trp	Asp	Val	Trp	Tyr	Cys	Phe		
		835					840						845				
His	Leu	Cys	Leu	Ala	Trp	Leu	Pro	Leu	Leu	Ala	Arg	Ser	Arg	Arg	Ser		
	850					855					860						
Ala	Gln	Thr	Leu	Pro	Tyr	Asp	Ala	Phe	Val	Val	Phe	Asp	Lys	Ala	Gln		
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			885						890						895		
Glu	Arg	Arg	Gly	Arg	Arg	Ala	Leu	Arg	Leu	Cys	Leu	Glu	Asp	Arg	Asp		

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 Trp Leu Pro Gly Gln Thr Leu Phe Glu Asn Leu Trp Ala Ser Ile Tyr
 915 920 925
 Gly Ser Arg Lys Thr Leu Phe Val Leu Ala His Thr Asp Arg Val Ser
 930 935 940
 Gly Leu Leu Arg Thr Ser Phe Leu Leu Ala Gln Gln Arg Leu Leu Glu
 945 950 955 960
 Asp Arg Lys Asp Val Val Val Leu Val Ile Leu Arg Pro Asp Ala His
 965 970 975
 Arg Ser Arg Tyr Val Arg Leu Arg Gln Arg Leu Cys Arg Gln Ser Val
 980 985 990
 Leu Phe Trp Pro Gln Gln Pro Asn Gly Gln Gly Gly Phe Trp Ala Gln
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 tg 3002

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<400> 77

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 35 40 45
 Ala Thr Thr Thr Leu Asp Leu Ser Tyr Asn Leu Leu Phe Gln Leu Gln
 50 55 60
 Ser Ser Asp Phe His Ser Val Ser Lys Leu Arg Val Leu Ile Leu Cys
 65 70 75 80
 His Asn Arg Ile Gln Gln Leu Asp Leu Lys Thr Phe Glu Phe Asn Lys
 85 90 95
 Glu Leu Arg Tyr Leu Asp Leu Ser Asn Asn Arg Leu Lys Ser Val Thr
 100 105 110
 Trp Tyr Leu Leu Ala Gly Leu Arg Tyr Leu Asp Leu Ser Phe Asn Asp
 115 120 125
 Phe Asp Thr Met Pro Ile Cys Glu Glu Ala Gly Asn Met Ser His Leu
 130 135 140
 Glu Ile Leu Gly Leu Ser Gly Ala Lys Ile Gln Lys Ser Asp Phe Gln
 145 150 155 160
 Lys Ile Ala His Leu His Leu Asn Thr Val Phe Leu Gly Phe Arg Thr
 165 170 175
 Leu Pro His Tyr Glu Glu Gly Ser Leu Pro Ile Leu Asn Thr Thr Lys
 180 185 190
 Leu His Ile Val Leu Pro Met Asp Thr Asn Phe Trp Val Leu Leu Arg
 195 200 205
 Asp Gly Ile Lys Thr Ser Lys Ile Leu Glu Met Thr Asn Ile Asp Gly
 210 215 220
 Lys Ser Gln Phe Val Ser Tyr Glu Met Gln Arg Asn Leu Ser Leu Glu
 225 230 235 240

Asn Ala Lys Thr Ser Val Leu Leu Leu Asn Lys Val Asp Leu Leu Trp
 245 250 255
 Asp Asp Leu Phe Leu Ile Leu Gln Phe Val Trp His Thr Ser Val Glu
 260 265 270
 His Phe Gln Ile Arg Asn Val Thr Phe Gly Gly Lys Ala Tyr Leu Asp
 275 280 285
 His Asn Ser Phe Asp Tyr Ser Asn Thr Val Met Arg Thr Ile Lys Leu
 290 295 300
 Glu His Val His Phe Arg Val Phe Tyr Ile Gln Gln Asp Lys Ile Tyr
 305 310 315 320
 Leu Leu Leu Thr Lys Met Asp Ile Glu Asn Leu Thr Ile Ser Asn Ala
 325 330 335
 Gln Met Pro His Met Leu Phe Pro Asn Tyr Pro Thr Lys Phe Gln Tyr
 340 345 350
 Leu Asn Phe Ala Asn Asn Ile Leu Thr Asp Glu Leu Phe Lys Arg Thr
 355 360 365
 Ile Gln Leu Pro His Leu Lys Thr Leu Ile Leu Asn Gly Asn Lys Leu
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 Glu Thr Leu Ser Leu Val Ser Cys Phe Ala Asn Asn Thr Pro Leu Glu
 385 390 395 400
 His Leu Asp Leu Ser Gln Asn Leu Leu Gln His Lys Asn Asp Glu Asn
 405 410 415
 Cys Ser Trp Pro Glu Thr Val Val Asn Met Asn Leu Ser Tyr Asn Lys
 420 425 430
 Leu Ser Asp Ser Val Phe Arg Cys Leu Pro Lys Ser Ile Gln Ile Leu
 435 440 445
 Asp Leu Asn Asn Asn Gln Ile Gln Thr Val Pro Lys Glu Thr Ile His
 450 455 460
 Leu Met Ala Leu Arg Glu Leu Asn Ile Ala Phe Asn Phe Leu Thr Asp
 465 470 475 480
 Leu Pro Gly Cys Ser His Phe Ser Arg Leu Ser Val Leu Asn Ile Glu
 485 490 495
 Met Asn Phe Ile Leu Ser Pro Ser Leu Asp Phe Val Gln Ser Cys Gln
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 Glu Val Lys Thr Leu Asn Ala Gly Arg Asn Pro Phe Arg Cys Thr Cys
 515 520 525
 Glu Leu Lys Asn Phe Ile Gln Leu Glu Thr Tyr Ser Glu Val Met Met
 530 535 540
 Val Gly Trp Ser Asp Ser Tyr Thr Cys Glu Tyr Pro Leu Asn Leu Arg
 545 550 555 560
 Gly Ile Arg Leu Lys Asp Val His Leu His Glu Leu Ser Cys Asn Thr

565 570 575
 Ala Leu Leu Ile Val Thr Ile Val Val Ile Met Leu Val Leu Gly Leu
 580 585 590
 Ala Val Ala Phe Cys Cys Leu His Phe Asp Leu Pro Trp Tyr Leu Arg
 595 600 605
 Met Leu Gly Gln Cys Thr Gln Thr Trp His Arg Val Arg Lys Thr Thr
 610 615 620
 Gln Glu Gln Leu Lys Arg Asn Val Arg Phe His Ala Phe Ile Ser Tyr
 625 630 635 640
 Ser Glu His Asp Ser Leu Trp Val Lys Asn Glu Leu Ile Pro Asn Leu
 645 650 655
 Glu Lys Glu Asp Gly Ser Ile Leu Ile Cys Leu Tyr Glu Ser Tyr Phe
 660 665 670
 Asp Pro Gly Lys Ser Ile Ser Glu Asn Ile Val Ser Phe Ile Glu Lys
 675 680 685
 Ser Tyr Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Asn Glu
 690 695 700
 Trp Cys His Tyr Glu Phe Tyr Phe Ala His His Asn Leu Phe His Glu
 705 710 715 720
 Asn Ser Asp His Ile Ile Leu Ile Leu Leu Glu Pro Ile Pro Phe Tyr
 725 730 735
 Cys Ile Pro Thr Arg Tyr His Lys Leu Lys Ala Leu Leu Glu Lys Lys
 740 745 750
 Ala Tyr Leu Glu Trp Pro Lys Asp Arg Arg Lys Cys Gly Leu Phe Trp
 755 760 765
 Ala Asn Leu Arg Ala Ala Ile Asn Val Asn Val Leu Ala Thr Arg Glu
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Glu Phe Ala Val Asp Lys Ser Lys Arg Gly Leu Ile His Val Pro Lys
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Ala Glu Leu Gln Val Ser Asp Met Ser Phe Leu Ser Glu Leu Thr Val
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Leu Arg Leu Ser His Asn Arg Ile Gln Leu Leu Asp Leu Ser Val Phe
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Lys Phe Asn Gln Asp Leu Glu Tyr Leu Asp Leu Ser His Asn Gln Leu
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Gln Lys Ile Ser Cys His Pro Ile Val Ser Phe Arg His Leu Asp Leu
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 Ile Phe Glu Lys Cys Ser Thr Leu Val Lys Leu Glu Thr Leu Ile Leu
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 Ser Gly Arg His Lys Glu Asn Cys Thr Trp Val Glu Ser Ile Val Val
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 485 490 495
 Leu Ser Val Leu Ile Ile Asp His Asn Ser Val Ser His Pro Ser Ala
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 Ala Thr Met Leu Val Leu Ala Val Thr Val Thr Ser Leu Cys Ile Tyr
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 Lys Ser Glu Leu Val Pro Tyr Leu Glu Lys Glu Asp Ile Gln Ile Cys
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 Leu His Glu Arg Asn Phe Val Pro Gly Lys Ser Ile Val Glu Asn Ile
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 Glu Pro Ile Pro Gln Asn Ser Ile Pro Asn Lys Tyr His Lys Leu Lys
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 Ala Leu Met Thr Gln Arg Thr Tyr Leu Gln Trp Pro Lys Glu Lys Ser
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 Ala Glu Leu Gln Val Ser Asp Met Ser Phe Leu Ser Glu Leu Thr Val
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 Lys Phe Asn Gln Asp Leu Glu Tyr Leu Asp Leu Ser His Asn Gln Leu
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Gln Lys Ile Ser Cys His Pro Ile Val Ser Phe Arg His Leu Asp Leu
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 Ser Phe Asn Asp Phe Lys Ala Leu Pro Ile Cys Lys Glu Phe Gly Asn
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Gln Thr Ala Leu Tyr Thr Val Phe Ser Glu Met Asn Ile Met Met Leu
 325 330 335

Thr Ile Ser Asp Thr Pro Phe Ile His Met Leu Cys Pro His Ala Pro
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Ser Thr Phe Lys Phe Leu Asn Phe Thr Gln Asn Val Phe Thr Asp Ser
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Ile Phe Glu Lys Cys Ser Thr Leu Val Lys Leu Glu Thr Leu Ile Leu
 370 375 380

Gln Lys Asn Gly Leu Lys Asp Leu Phe Lys Val Gly Leu Met Thr Lys
 385 390 395 400

Asp Met Pro Ser Leu Glu Ile Leu Asp Val Ser Trp Asn Ser Leu Glu
 405 410 415

Ser Gly Arg His Lys Glu Asn Cys Thr Trp Val Glu Ser Ile Val Val
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Leu Asn Leu Ser Ser Asn Met Leu Thr Asp Ser Val Phe Arg Cys Leu
 435 440 445

Pro Pro Arg Ile Lys Val Leu Asp Leu His Ser Asn Lys Ile Lys Ser
 450 455 460

Val Pro Lys Gln Val Val Lys Leu Glu Ala Leu Gln Glu Leu Asn Val
 465 470 475 480

Ala Phe Asn Ser Leu Thr Asp Leu Pro Gly Cys Gly Ser Phe Ser Ser
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Leu Ser Val Leu Ile Ile Asp His Asn Ser Val Ser His Pro Ser Ala
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Asn Pro Phe Gln Cys Thr Cys Glu Leu Arg Glu Phe Val Lys Asn Ile
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Asp Gln Val Ser Ser Glu Val Leu Glu Gly Trp Pro Asp Ser Tyr Lys
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Cys Asp Tyr Pro Glu Ser Tyr Arg Gly Ser Pro Leu Lys Asp Phe His
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 <213> murine

<400> 84
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 <211> 2421
 <212> DNA
 <213> murine

<400> 85	
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aatgaacttg	agtctatggg agactattca aacaggaacc ttactcatgt ccccaaagac 180
ctgccacca	gaacaaaagc cctgagtctg tctcaaaact ctatatctga gcttcggatg 240
cctgatata	gccttctgtc agagctgaga gttctgagac tctcccacaa caggatacgg 300
agccttgatt	tccatgtatt cttgttcaat caggacttag aatacctgga tgtctcacac 360
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2421

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<211> 806

<212> PRT

<213> murine

<400> 86

Met Val Lys Ser Leu Trp Asp Ser Leu Cys Asn Met Ser Gln Asp Arg
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Lys Pro Ile Val Gly Ser Phe His Phe Val Cys Ala Leu Ala Leu Ile
 20 25 30

Val Gly Ser Met Thr Pro Phe Ser Asn Glu Leu Glu Ser Met Val Asp
 35 40 45

Tyr Ser Asn Arg Asn Leu Thr His Val Pro Lys Asp Leu Pro Pro Arg
 50 55 60

Thr Lys Ala Leu Ser Leu Ser Gln Asn Ser Ile Ser Glu Leu Arg Met
 65 70 75 80

Pro Asp Ile Ser Phe Leu Ser Glu Leu Arg Val Leu Arg Leu Ser His
 85 90 95

Asn Arg Ile Arg Ser Leu Asp Phe His Val Phe Leu Phe Asn Gln Asp
 100 105 110

Leu Glu Tyr Leu Asp Val Ser His Asn Arg Leu Gln Asn Ile Ser Cys
 115 120 125

Cys Pro Met Ala Ser Leu Arg His Leu Asp Leu Ser Phe Asn Asp Phe
 130 135 140

Asp Val Leu Pro Val Cys Lys Glu Phe Gly Asn Leu Thr Lys Leu Thr
 145 150 155 160

Phe Leu Gly Leu Ser Ala Ala Lys Phe Arg Gln Leu Asp Leu Leu Pro
 165 170 175

Val Ala His Leu His Leu Ser Cys Ile Leu Leu Asp Leu Val Ser His
 180 185 190

His Ile Lys Gly Gly Glu Thr Glu Ser Leu Gln Ile Pro Asn Thr Thr
 195 200 205

Val Leu His Leu Val Phe His Pro Asn Ser Leu Phe Ser Val Gln Val
 210 215 220

Asn Met Ser Val Asn Ala Leu Gly His Leu Gln Leu Ser Asn Ile Lys
 225 230 235 240

Leu Asn Asp Glu Asn Cys Gln Arg Leu Met Thr Phe Leu Ser Glu Leu
 245 250 255

Thr Arg Gly Pro Thr Leu Leu Asn Val Thr Leu Gln His Ile Glu Thr
 260 265 270

Thr Trp Lys Cys Ser Val Lys Leu Phe Gln Phe Phe Trp Pro Arg Pro
 275 280 285
 Val Glu Tyr Leu Asn Ile Tyr Asn Leu Thr Ile Thr Glu Arg Ile Asp
 290 295 300
 Arg Glu Glu Phe Thr Tyr Ser Glu Thr Ala Leu Lys Ser Leu Met Ile
 305 310 315 320
 Glu His Val Lys Asn Gln Val Phe Leu Phe Ser Lys Glu Ala Leu Tyr
 325 330 335
 Ser Val Phe Ala Glu Met Asn Ile Lys Met Leu Ser Ile Ser Asp Thr
 340 345 350
 Pro Phe Ile His Met Val Cys Pro Pro Ser Pro Ser Ser Phe Thr Phe
 355 360 365
 Leu Asn Phe Thr Gln Asn Val Phe Thr Asp Ser Val Phe Gln Gly Cys
 370 375 380
 Ser Thr Leu Lys Arg Leu Gln Thr Leu Ile Leu Gln Arg Asn Gly Leu
 385 390 395 400
 Lys Asn Phe Phe Lys Val Ala Leu Met Thr Lys Asn Met Ser Ser Leu
 405 410 415
 Glu Thr Leu Asp Val Ser Leu Asn Ser Leu Asn Ser His Ala Tyr Asp
 420 425 430
 Arg Thr Cys Ala Trp Ala Glu Ser Ile Leu Val Leu Asn Leu Ser Ser
 435 440 445
 Asn Met Leu Thr Gly Ser Val Phe Arg Cys Leu Pro Pro Lys Val Lys
 450 455 460
 Val Leu Asp Leu His Asn Asn Arg Ile Met Ser Ile Pro Lys Asp Val
 465 470 475 480
 Thr His Leu Gln Ala Leu Gln Glu Leu Asn Val Ala Ser Asn Ser Leu
 485 490 495
 Thr Asp Leu Pro Gly Cys Gly Ala Phe Ser Ser Leu Ser Val Leu Val
 500 505 510
 Ile Asp His Asn Ser Val Ser His Pro Ser Glu Asp Phe Phe Gln Ser
 515 520 525
 Cys Gln Asn Ile Arg Ser Leu Thr Ala Gly Asn Asn Pro Phe Gln Cys
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 Thr Cys Glu Leu Arg Asp Phe Val Lys Asn Ile Gly Trp Val Ala Arg
 545 550 555 560
 Glu Val Val Glu Gly Trp Pro Asp Ser Tyr Arg Cys Asp Tyr Pro Glu
 565 570 575
 Ser Ser Lys Gly Thr Ala Leu Arg Asp Phe His Met Ser Pro Leu Ser
 580 585 590
 Cys Asp Thr Val Leu Leu Thr Val Thr Ile Gly Ala Thr Met Leu Val

595 600 605
 Leu Ala Val Thr Gly Ala Phe Leu Cys Leu Tyr Phe Asp Leu Pro Trp
 610 615 620
 Tyr Val Arg Met Leu Cys Gln Trp Thr Gln Thr Arg His Arg Ala Arg
 625 630 635 640
 His Ile Pro Leu Glu Glu Leu Gln Arg Asn Leu Gln Phe His Ala Phe
 645 650 655
 Val Ser Tyr Ser Glu His Asp Ser Ala Trp Val Lys Asn Glu Leu Leu
 660 665 670
 Pro Asn Leu Glu Lys Asp Asp Ile Arg Val Cys Leu His Glu Arg Asn
 675 680 685
 Phe Val Pro Gly Lys Ser Ile Val Glu Asn Ile Ile Asn Phe Ile Glu
 690 695 700
 Lys Ser Tyr Lys Ala Ile Phe Val Leu Ser Pro His Phe Ile Gln Ser
 705 710 715 720
 Glu Trp Cys His Tyr Glu Leu Tyr Phe Ala His His Asn Leu Phe His
 725 730 735
 Glu Gly Ser Asp Asn Leu Ile Leu Ile Leu Leu Glu Pro Ile Leu Gln
 740 745 750
 Asn Asn Ile Pro Ser Arg Tyr His Lys Leu Arg Ala Leu Met Ala Gln
 755 760 765
 Arg Thr Tyr Leu Glu Trp Pro Thr Glu Lys Gly Lys Arg Gly Leu Phe
 770 775 780
 Trp Ala Asn Leu Arg Ala Ser Phe Ile Met Lys Leu Ala Leu Val Asn
 785 790 795 800
 Glu Asp Asp Val Lys Thr
 805

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 <211> 806
 <212> PRT
 <213> murine

<400> 87

Met Val Lys Ser Leu Trp Asp Ser Leu Cys Asn Met Ser Gln Asp Arg
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 Lys Pro Ile Val Gly Ser Phe His Phe Val Cys Ala Leu Ala Leu Ile
 20 25 30
 Val Gly Ser Met Thr Pro Phe Ser Asn Glu Leu Glu Ser Met Val Asp
 35 40 45
 Tyr Ser Asn Arg Asn Leu Thr His Val Pro Lys Asp Leu Pro Pro Arg
 50 55 60
 Thr Lys Ala Leu Ser Leu Ser Gln Asn Ser Ile Ser Glu Leu Arg Met
 65 70 75 80

Pro Asp Ile Ser Phe Leu Ser Glu Leu Arg Val Leu Arg Leu Ser His
 85 90 95
 Asn Arg Ile Arg Ser Leu Asp Phe His Val Phe Leu Phe Asn Gln Asp
 100 105 110
 Leu Glu Tyr Leu Asp Val Ser His Asn Arg Leu Gln Asn Ile Ser Cys
 115 120 125
 Cys Pro Met Ala Ser Leu Arg His Leu Asp Leu Ser Phe Asn Asp Phe
 130 135 140
 Asp Val Leu Pro Val Cys Lys Glu Phe Gly Asn Leu Thr Lys Leu Thr
 145 150 155 160
 Phe Leu Gly Leu Ser Ala Ala Lys Phe Arg Gln Leu Asp Leu Leu Pro
 165 170 175
 Val Ala His Leu His Leu Ser Cys Ile Leu Leu Asp Leu Val Ser Tyr
 180 185 190
 His Ile Lys Gly Gly Glu Thr Glu Ser Leu Gln Ile Pro Asn Thr Thr
 195 200 205
 Val Leu His Leu Val Phe His Pro Asn Ser Leu Phe Ser Val Gln Val
 210 215 220
 Asn Met Ser Val Asn Ala Leu Gly His Leu Gln Leu Ser Asn Ile Lys
 225 230 235 240
 Leu Asn Asp Glu Asn Cys Gln Arg Leu Met Thr Phe Leu Ser Glu Leu
 245 250 255
 Thr Arg Gly Pro Thr Leu Leu Asn Val Thr Leu Gln His Ile Glu Thr
 260 265 270
 Thr Trp Lys Cys Ser Val Lys Leu Phe Gln Phe Phe Trp Pro Arg Pro
 275 280 285
 Val Glu Tyr Leu Asn Ile Tyr Asn Leu Thr Ile Thr Glu Arg Ile Asp
 290 295 300
 Arg Glu Glu Phe Thr Tyr Ser Glu Thr Ala Leu Lys Ser Leu Met Ile
 305 310 315 320
 Glu His Val Lys Asn Gln Val Phe Leu Phe Ser Lys Glu Ala Leu Tyr
 325 330 335
 Ser Val Phe Ala Glu Met Asn Ile Lys Met Leu Ser Ile Ser Asp Thr
 340 345 350
 Pro Phe Ile His Met Val Cys Pro Pro Ser Pro Ser Ser Phe Thr Phe
 355 360 365
 Leu Asn Phe Thr Gln Asn Val Phe Thr Asp Ser Val Phe Gln Gly Cys
 370 375 380
 Ser Thr Leu Lys Arg Leu Gln Thr Leu Ile Leu Gln Arg Asn Gly Leu
 385 390 395 400
 Lys Asn Phe Phe Lys Val Ala Leu Met Thr Lys Asn Met Ser Ser Leu

405 410 415
 Glu Thr Leu Asp Val Ser Leu Asn Ser Leu Asn Ser His Ala Tyr Asp
 420 425 430
 Arg Thr Cys Ala Trp Ala Glu Ser Ile Leu Val Leu Asn Leu Ser Ser
 435 440 445
 Asn Met Leu Thr Gly Ser Val Phe Arg Cys Leu Pro Pro Lys Val Lys
 450 455 460
 Val Leu Asp Leu His Asn Asn Arg Ile Met Ser Ile Pro Lys Asp Val
 465 470 475 480
 Thr His Leu Gln Ala Leu Gln Glu Leu Asn Val Ala Ser Asn Ser Leu
 485 490 495
 Thr Asp Leu Pro Gly Cys Gly Ala Phe Ser Ser Leu Ser Val Leu Val
 500 505 510
 Ile Asp His Asn Ser Val Ser His Pro Ser Glu Asp Phe Phe Gln Ser
 515 520 525
 Cys Gln Asn Ile Arg Ser Leu Thr Ala Gly Asn Asn Pro Phe Gln Cys
 530 535 540
 Thr Cys Glu Leu Arg Asp Phe Val Lys Asn Ile Gly Trp Val Ala Arg
 545 550 555 560
 Glu Val Val Glu Gly Trp Pro Asp Ser Tyr Arg Cys Asp Tyr Pro Glu
 565 570 575
 Ser Ser Lys Gly Thr Ala Leu Arg Asp Phe His Met Ser Pro Leu Ser
 580 585 590
 Cys Asp Thr Val Leu Leu Thr Val Thr Ile Gly Ala Thr Met Leu Val
 595 600 605
 Leu Ala Val Thr Gly Ala Phe Leu Cys Leu Tyr Phe Asp Leu Pro Trp
 610 615 620
 Tyr Val Arg Met Leu Cys Gln Trp Thr Gln Thr Arg His Arg Ala Arg
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 His Ile Pro Leu Glu Glu Leu Gln Arg Asn Leu Gln Phe His Ala Phe
 645 650 655
 Val Ser Tyr Ser Glu His Asp Ser Ala Trp Val Lys Asn Glu Leu Leu
 660 665 670
 Pro Asn Leu Glu Lys Asp Asp Ile Arg Val Cys Leu His Glu Arg Asn
 675 680 685
 Phe Val Pro Gly Lys Ser Ile Val Glu Asn Ile Ile Asn Phe Ile Glu
 690 695 700
 Lys Ser Tyr Lys Ala Ile Phe Val Leu Ser Pro His Phe Ile Gln Ser
 705 710 715 720
 Glu Trp Cys His Tyr Glu Leu Tyr Phe Ala His His Asn Leu Phe His
 725 730 735
 Glu Gly Ser Asp Asn Leu Ile Leu Ile Leu Leu Glu Pro Ile Leu Gln

740 745 750
 Asn Asn Ile Pro Ser Arg Tyr His Lys Leu Arg Ala Leu Met Ala Gln
 755 760 765
 Arg Thr Tyr Leu Glu Trp Pro Thr Glu Lys Gly Lys Arg Gly Leu Phe
 770 775 780
 Trp Ala Asn Leu Arg Ala Ser Phe Ile Met Lys Leu Ala Leu Val Asn
 785 790 795 800
 Glu Asp Asp Val Lys Thr
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<210> 88
 <211> 806
 <212> PRT
 <213> murine

<400> 88

Met Val Lys Ser Leu Trp Asp Ser Leu Cys Asn Met Ser Gln Asp Arg
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 Lys Pro Ile Val Gly Ser Phe His Phe Val Cys Ala Leu Ala Leu Ile
 20 25 30
 Val Gly Ser Met Thr Pro Phe Ser Asn Glu Leu Glu Ser Met Val Asp
 35 40 45
 Tyr Ser Asn Arg Asn Leu Thr His Val Pro Lys Asp Leu Pro Pro Arg
 50 55 60
 Thr Lys Ala Leu Ser Leu Ser Gln Asn Ser Ile Ser Glu Leu Arg Met
 65 70 75 80
 Pro Asp Ile Ser Phe Leu Ser Glu Leu Arg Val Leu Arg Leu Ser His
 85 90 95
 Asn Arg Ile Arg Ser Leu Asp Phe His Val Phe Leu Phe Asn Gln Asp
 100 105 110
 Leu Glu Tyr Leu Asp Val Ser His Asn Arg Leu Gln Asn Ile Ser Cys
 115 120 125
 Cys Pro Met Ala Ser Leu Arg His Leu Asp Leu Ser Phe Asn Asp Phe
 130 135 140
 Asp Val Leu Pro Val Cys Lys Glu Phe Gly Asn Leu Thr Lys Leu Thr
 145 150 155 160
 Phe Leu Gly Leu Ser Ala Ala Lys Phe Arg Gln Leu Asp Leu Leu Pro
 165 170 175
 Val Ala His Leu His Leu Ser Cys Ile Leu Leu Asp Leu Val Ser His
 180 185 190
 His Ile Lys Gly Gly Glu Thr Glu Ser Leu Gln Ile Pro Asn Thr Thr
 195 200 205
 Val Leu His Leu Val Phe His Pro Asn Ser Leu Phe Ser Val Gln Val
 210 215 220

Asn Met Ser Val Asn Ala Leu Gly His Leu Gln Leu Ser Asn Ile Lys
 225 230 235 240
 Leu Asn Asp Glu Asn Cys Gln Arg Leu Met Thr Phe Leu Ser Glu Leu
 245 250 255
 Thr Arg Gly Pro Thr Leu Leu Asn Val Thr Leu Gln His Ile Glu Thr
 260 265 270
 Thr Trp Lys Cys Ser Val Lys Leu Phe Gln Phe Phe Trp Pro Arg Pro
 275 280 285
 Val Glu Tyr Leu Asn Ile Tyr Asn Leu Thr Ile Thr Glu Arg Ile Asp
 290 295 300
 Arg Glu Glu Phe Thr Tyr Ser Glu Thr Ala Leu Lys Ser Leu Met Ile
 305 310 315 320
 Glu His Val Lys Asn Gln Val Phe Leu Phe Ser Lys Glu Ala Leu Tyr
 325 330 335
 Ser Val Phe Ala Glu Met Asn Ile Lys Met Leu Ser Ile Ser Asp Thr
 340 345 350
 Pro Phe Ile His Met Val Cys Pro Pro Ser Pro Ser Ser Phe Thr Phe
 355 360 365
 Leu Asn Phe Thr Gln Asn Val Phe Thr Asp Ser Val Phe Gln Gly Cys
 370 375 380
 Ser Thr Leu Lys Arg Leu Gln Thr Leu Ile Leu Gln Arg Asn Gly Leu
 385 390 395 400
 Lys Asn Phe Phe Lys Val Ala Leu Met Thr Lys Asn Met Ser Ser Leu
 405 410 415
 Glu Thr Leu Asp Val Ser Leu Asn Ser Leu Asn Ser His Ala Tyr Asp
 420 425 430
 Arg Thr Cys Ala Trp Ala Glu Ser Ile Leu Val Leu Asn Leu Ser Ser
 435 440 445
 Asn Met Leu Thr Gly Ser Val Phe Arg Cys Leu Pro Pro Lys Val Lys
 450 455 460
 Val Leu Asp Leu His Asn Asn Arg Ile Met Ser Ile Pro Lys Asp Val
 465 470 475 480
 Thr His Leu Gln Ala Leu Gln Glu Leu Asn Val Ala Ser Asn Ser Leu
 485 490 495
 Thr Asp Leu Pro Gly Cys Gly Ala Phe Ser Ser Leu Ser Val Leu Val
 500 505 510
 Ile Asp His Asn Ser Val Ser His Pro Ser Glu Asp Phe Phe Gln Ser
 515 520 525
 Cys Gln Asn Ile Arg Ser Leu Thr Ala Gly Asn Asn Pro Phe Gln Cys
 530 535 540
 Thr Cys Glu Leu Arg Asp Phe Val Lys Asn Ile Gly Trp Val Ala Arg

545 550 555 560
 Glu Val Val Glu Gly Trp Pro Asp Ser Tyr Arg Cys Asp Tyr Pro Glu
 565 570 575

 Ser Ser Lys Gly Thr Ala Leu Arg Asp Phe His Met Ser Pro Leu Ser
 580 585 590

 Cys Asp Thr Val Leu Leu Thr Val Thr Ile Gly Ala Thr Met Leu Val
 595 600 605

 Leu Ala Val Thr Gly Ala Phe Leu Cys Leu Tyr Phe Asp Leu Pro Trp
 610 615 620

 Tyr Val Arg Met Leu Cys Gln Trp Thr Gln Thr Arg His Arg Ala Arg
 625 630 635 640

 His Ile Pro Leu Glu Glu Leu Gln Arg Asn Leu Gln Phe His Ala Phe
 645 650 655

 Val Ser Tyr Ser Glu His Asp Ser Ala Trp Val Lys Asn Glu Leu Leu
 660 665 670

 Pro Asn Leu Glu Lys Asp Asp Ile Arg Val Cys Leu His Glu Arg Asn
 675 680 685

 Phe Val Pro Gly Lys Ser Ile Val Glu Asn Ile Ile Asn Phe Ile Glu
 690 695 700

 Lys Ser Tyr Lys Ala Ile Phe Val Leu Ser Pro His Phe Ile Gln Ser
 705 710 715 720

 Glu Trp Cys His Tyr Glu Leu Tyr Phe Ala His His Asn Leu Phe His
 725 730 735

 Glu Gly Ser Asp Asn Leu Ile Leu Ile Leu Leu Glu Pro Ile Leu Gln
 740 745 750

 Asn Asn Ile Pro Ser Arg Tyr His Lys Leu Arg Ala Leu Met Ala Gln
 755 760 765

 Arg Thr Tyr Leu Glu Trp Pro Thr Glu Lys Gly Lys Arg Gly Leu Phe
 770 775 780

 Trp Ala Asn Leu Arg Ala Ser Phe Ile Met Lys Leu Ala Leu Val Asn
 785 790 795 800

 Glu Asp Asp Val Lys Thr
 805

<210> 89
 <211> 795
 <212> PRT
 <213> murine

<400> 89

Met Ser Gln Asp Arg Lys Pro Ile Val Gly Ser Phe His Phe Val Cys
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 Ala Leu Ala Leu Ile Val Gly Ser Met Thr Pro Phe Ser Asn Glu Leu
 20 25 30

Glu Ser Met Val Asp Tyr Ser Asn Arg Asn Leu Thr His Val Pro Lys
 35 40 45
 Asp Leu Pro Pro Arg Thr Lys Ala Leu Ser Leu Ser Gln Asn Ser Ile
 50 55 60
 Ser Glu Leu Arg Met Pro Asp Ile Ser Phe Leu Ser Glu Leu Arg Val
 65 70 75 80
 Leu Arg Leu Ser His Asn Arg Ile Arg Ser Leu Asp Phe His Val Phe
 85 90 95
 Leu Phe Asn Gln Asp Leu Glu Tyr Leu Asp Val Ser His Asn Arg Leu
 100 105 110
 Gln Asn Ile Ser Cys Cys Pro Met Ala Ser Leu Arg His Leu Asp Leu
 115 120 125
 Ser Phe Asn Asp Phe Asp Val Leu Pro Val Cys Lys Glu Phe Gly Asn
 130 135 140
 Leu Thr Lys Leu Thr Phe Leu Gly Leu Ser Ala Ala Lys Phe Arg Gln
 145 150 155 160
 Leu Asp Leu Leu Pro Val Ala His Leu His Leu Ser Cys Ile Leu Leu
 165 170 175
 Asp Leu Val Ser Tyr His Ile Lys Gly Gly Glu Thr Glu Ser Leu Gln
 180 185 190
 Ile Pro Asn Thr Thr Val Leu His Leu Val Phe His Pro Asn Ser Leu
 195 200 205
 Phe Ser Val Gln Val Asn Met Ser Val Asn Ala Leu Gly His Leu Gln
 210 215 220
 Leu Ser Asn Ile Lys Leu Asn Asp Glu Asn Cys Gln Arg Leu Met Thr
 225 230 235 240
 Phe Leu Ser Glu Leu Thr Arg Gly Pro Thr Leu Leu Asn Val Thr Leu
 245 250 255
 Gln His Ile Glu Thr Thr Trp Lys Cys Ser Val Lys Leu Phe Gln Phe
 260 265 270
 Phe Trp Pro Arg Pro Val Glu Tyr Leu Asn Ile Tyr Asn Leu Thr Ile
 275 280 285
 Thr Glu Arg Ile Asp Arg Glu Glu Phe Thr Tyr Ser Glu Thr Ala Leu
 290 295 300
 Lys Ser Leu Met Ile Glu His Val Lys Asn Gln Val Phe Leu Phe Ser
 305 310 315 320
 Lys Glu Ala Leu Tyr Ser Val Phe Ala Glu Met Asn Ile Lys Met Leu
 325 330 335
 Ser Ile Ser Asp Thr Pro Phe Ile His Met Val Cys Pro Pro Ser Pro
 340 345 350
 Ser Ser Phe Thr Phe Leu Asn Phe Thr Gln Asn Val Phe Thr Asp Ser

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      355      360      365
Val Phe Gln Gly Cys Ser Thr Leu Lys Arg Leu Gln Thr Leu Ile Leu
    370      375      380

Gln Arg Asn Gly Leu Lys Asn Phe Phe Lys Val Ala Leu Met Thr Lys
385      390      395      400

Asn Met Ser Ser Leu Glu Thr Leu Asp Val Ser Leu Asn Ser Leu Asn
      405      410      415

Ser His Ala Tyr Asp Arg Thr Cys Ala Trp Ala Glu Ser Ile Leu Val
      420      425      430

Leu Asn Leu Ser Ser Asn Met Leu Thr Gly Ser Val Phe Arg Cys Leu
      435      440      445

Pro Pro Lys Val Lys Val Leu Asp Leu His Asn Asn Arg Ile Met Ser
      450      455      460

Ile Pro Lys Asp Val Thr His Leu Gln Ala Leu Gln Glu Leu Asn Val
465      470      475      480

Ala Ser Asn Ser Leu Thr Asp Leu Pro Gly Cys Gly Ala Phe Ser Ser
      485      490      495

Leu Ser Val Leu Val Ile Asp His Asn Ser Val Ser His Pro Ser Glu
      500      505      510

Asp Phe Phe Gln Ser Cys Gln Asn Ile Arg Ser Leu Thr Ala Gly Asn
      515      520      525

Asn Pro Phe Gln Cys Thr Cys Glu Leu Arg Asp Phe Val Lys Asn Ile
      530      535      540

Gly Trp Val Ala Arg Glu Val Val Glu Gly Trp Pro Asp Ser Tyr Arg
545      550      555      560

Cys Asp Tyr Pro Glu Ser Ser Lys Gly Thr Ala Leu Arg Asp Phe His
      565      570      575

Met Ser Pro Leu Ser Cys Asp Thr Val Leu Leu Thr Val Thr Ile Gly
      580      585      590

Ala Thr Met Leu Val Leu Ala Val Thr Gly Ala Phe Leu Cys Leu Tyr
      595      600      605

Phe Asp Leu Pro Trp Tyr Val Arg Met Leu Cys Gln Trp Thr Gln Thr
      610      615      620

Arg His Arg Ala Arg His Ile Pro Leu Glu Glu Leu Gln Arg Asn Leu
625      630      635      640

Gln Phe His Ala Phe Val Ser Tyr Ser Glu His Asp Ser Ala Trp Val
      645      650      655

Lys Asn Glu Leu Leu Pro Asn Leu Glu Lys Asp Asp Ile Arg Val Cys
      660      665      670

Leu His Glu Arg Asn Phe Val Pro Gly Lys Ser Ile Val Glu Asn Ile
      675      680      685

Ile Asn Phe Ile Glu Lys Ser Tyr Lys Ala Ile Phe Val Leu Ser Pro

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        690                695                700
His Phe Ile Gln Ser Glu Trp Cys His Tyr Glu Leu Tyr Phe Ala His
705                710                715                720

His Asn Leu Phe His Glu Gly Ser Asp Asn Leu Ile Leu Ile Leu Leu
        725                730                735

Glu Pro Ile Leu Gln Asn Asn Ile Pro Ser Arg Tyr His Lys Leu Arg
        740                745                750

Ala Leu Met Ala Gln Arg Thr Tyr Leu Glu Trp Pro Thr Glu Lys Gly
        755                760                765

Lys Arg Gly Leu Phe Trp Ala Asn Leu Arg Ala Ser Phe Ile Met Lys
        770                775                780

Leu Ala Leu Val Asn Glu Asp Asp Val Lys Thr
785                790                795

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<220>

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<223> consensus p50 subunit

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<223> N = c or t

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<400> 90
ggggatnccc

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10

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<210> 91
<211> 10
<212> DNA
<213> artificial sequence

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<220>

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<223> consensus p65 subunit

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<220>
<221> misc_feature
<222> (4)..(4)
<223> N = a or g

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<220>
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<222> (5)..(5)
<223> N = a, c, g, or t

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<400> 91
gggnntttcc

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10

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<210> 92

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<211> 22
<212> DNA
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<223> consensus subunit

<400> 92
agttgagggg actttcccag gc

22

<210> 93
<211> 27
<212> DNA
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<220>

<223> CREB binding site

<400> 93
agagattgcc tgacgtcaga gagctag

27

<210> 94
<211> 21
<212> DNA
<213> artificial sequence

<220>

<223> AP-1 binding site

<400> 94
cgcttgatga gtcagccgga a

21

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<220>

<223> AP-1 binding site

<400> 95
cgcatgagtc agaca

15

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<223> ISRE

<400> 96

19
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<220>

<223> ISRE

<400> 97
agaacgaaac a 11

<210> 98
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<223> ISRE

<400> 98
gagaagtgaa agtgg 15

<210> 99
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<220>

<223> ISRE

<400> 99
taagaacatg aaactgaa 18

<210> 100
<211> 15
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<220>

<223> ISRE

<400> 100
atgaaactga aagta 15

<210> 101
<211> 16
<212> DNA
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<220>

<223> ISRE

<400> 101
tgaaaaccga aagcgc 16

<210> 102
<211> 13
<212> DNA
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<220>

<223> ISRE

<400> 102
agaaatggaa agt 13

<210> 103
<211> 9
<212> DNA
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<220>

<223> SRE

<400> 103
tcacccac 9

<210> 104
<211> 10
<212> DNA
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<220>

<223> SRE

<400> 104
ctcacccac 10

<210> 105
<211> 10
<212> DNA
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<220>

<223> SRE

<400> 105
gccaccctac 10

<210> 106
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<220>
<223> NFAT

<400> 106
tatgaaacag tttttcc 17

<210> 107
<211> 9
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<220>

<223> NFAT

<400> 107
aggaaactc 9

<210> 108
<211> 10
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<220>

<223> NFAT

<220>
<221> misc_feature
<222> (2)..(2)
<223> N = a or g

<220>
<221> misc_feature
<222> (5)..(5)
<223> N = a or g

<400> 108
anganattcc 10

<210> 109
<211> 16
<212> DNA
<213> artificial sequence

<220>

<223> NFAT

<400> 109
ccagttgagc cagaga 16

<210> 110
<211> 30
<212> DNA
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<220>

<223> GAS

<400> 110

ctttcagttt catattactc taaatccatt

30

<210> 111

<211> 10

<212> DNA

<213> artificial sequence

<220>

<223> p53 consensus site

<220>

<221> misc_feature

<222> (1)..(3)

<223> N = a or g

<220>

<221> misc_feature

<222> (5)..(6)

<223> N = a or t

<220>

<221> misc_feature

<222> (8)..(10)

<223> N = c or t

<400> 111

nnncnngnnn

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<210> 112

<211> 10

<212> DNA

<213> artificial sequence

<220>

<223> p53 consensus site

<400> 112

aggcatgcct

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<210> 113

<211> 10

<212> DNA

<213> artificial sequence

<220>

<223> p53 consensus site

<400> 113

gggcttgccc

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<210> 114

<211> 10
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<223> p53 consensus site

<400> 114
gggcttgctt 10

<210> 115
<211> 13
<212> DNA
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<220>

<223> p53 consensus site

<400> 115
gcctggactt gcc 13

<210> 116
<211> 20
<212> DNA
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<220>

<223> p53 consensus site

<400> 116
ggacatgccc gggcatgtcc 20

<210> 117
<211> 23
<212> DNA
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<220>

<223> p53 consensus site

<400> 117
gtagcattag cccagacatg tcc 23

<210> 118
<211> 36
<212> DNA
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<220>

<223> TARE

<400> 118
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 <211> 10
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<220>

<223> SRF

<220>
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 <222> (3)..(8)
 <223> N = a or t

<400> 119
 ccnnnnnnngg 10

<210> 120
 <211> 11
 <212> DNA
 <213> artificial sequence

<220>

<223> SRF

<400> 120
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<210> 121
 <211> 670
 <212> DNA
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<400> 121
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 aattatattc atattattaa tgtgtatcta tatagatttt tattttgcat atgtactttg 120
 atacaaaatt tacatgaaca aattacacta aaagttattc caaaaatata cttatcaaatt 180
 taagttaaatt gtcaatagct tttaaactta aatttttagtt taacttttct gtcattcttt 240
 actttgaata aaaagagcaa actttgtagt ttttatctgt gaagtagagg tatacgtaat 300
 atacataaat agatatgcca aatctgtgtt attaaaat tcatgaagatt tcaattagaa 360
 aaaaatacca taaaaggctt tgagtgcagg tgaaaaatag gcaatgatga aaaaaaatga 420
 aaaacttttt aaacacatgt agagagtgcg taaagaaagc aaaaacagag atagaaagta 480
 caactagggga atttagaaaa tggaaattag tatgttcact atttaagacc tatgcacaga 540
 gcaaagtctt cagaaaacct agaggccgaa gttcaagggt atccatctca agtagcctag 600
 caatatttgc aacatcccaa tggccctgtc cttttcttta ctgatggccg tgctgggtgct 660
 cagctacaaa 670

<210> 122
 <211> 207
 <212> DNA
 <213> Homo sapiens

<400> 122
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 catgagttta gagccgtgtt tctcaaatga tgggctagca cgcgtaagag ctcggtacct 180
 atcgatagag aaatgttctg gcacctg 207

<210> 123
 <211> 161
 <212> DNA
 <213> Homo sapiens

<400> 123
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 ctttctta at gcttctggac cactttccat ttctgttttt gctttccttc ttgaactctt 120
 tacatgagtt tagagccgtg tttctcaacc attttgtttt t 161

<210> 124
 <211> 300
 <212> DNA
 <213> Homo sapiens

<400> 124
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 tcattcactg aaacttttaa aaacattaga aaacctcaca gtttgtaa at ctttttccct 120
 attatatata tcataagata ggagcttaaa taaagagttt tagaaactac taaaatgtaa 180
 atgacatagg aaaactgaaa gggagaagtg aaagtgggaa attcctctga atagagagag 240
 gaccatctca tataaatagg ccataccac ggagaaagga cattctaact gcaacctttc 300

<210> 125
 <211> 401
 <212> DNA
 <213> Homo sapiens

<400> 125
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 cagtgaactc tgatcctgtc ctaactgcc a ctccttggtg tcccaagaaa gcggttcct 120
 gctctctgag gaggaccctc tccctggaag gtaaaactaa ggatgtcagc agagaaattt 180
 ttccaccatt ggtgcttggc caaagaggaa actgatgagc tcactctaga tgagagagca 240
 gtgagggaga gacagagact cgaatttccg gagctatttc agttttcttt tccgttttgt 300

gcaatttcac ttatgatacc ggccaatgct tggttgctat tttggaaact ccccttaggg 360
 gatgccctc aactggccct ataaagggcc agcctgagct g 401

<210> 126
 <211> 781
 <212> DNA
 <213> Homo sapiens

<400> 126
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 tatcatctcc ccaggtctgt gtctgtatga aatgtgcatg ggtgtgtgtg tgcacgcgtg 180
 tgttcccact cggggaatgt ggggagaggt gcatggagcc aagatgggtg gtaaatagta 240
 tgttttctgaa attaaaggac taatgtggag gaaggcgccc cagatgtact aaaccctttg 300
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 ttcttcctcg atctgtggaa cccagggaaat ctgcctagtg ctgtctccaa gcaccttggc 480
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 tcatttcctc ttagttcatt acctgggatt ttgatgtcta tgttccctcc tegtattga 600
 tacacacaca gagagagaca aacaaaaaag gaacttcttg aaattccccc agaaggtttt 660
 gagagttggt ttcaatgttg caacaagtca gtttctagtt taagtttcca tcagaaagga 720
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<210> 127
 <211> 277
 <212> DNA
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<400> 127
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 aaaaaggaac ttcttgaaat tccccagaa ggttttgaga gttgttttca atgttgcaac 180
 aagtcagttt ctagtttaag tttccatcag aaaggagtag agtatataag ttccagtacc 240
 agcaacagca gcagaagaaa caacatctgt ttcaggg 277

<210> 128
 <211> 305
 <212> DNA
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<400> 128

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tgcgatgcta	aaggacgtca	ttgcacaatc	ttaataaggt	ttccaatcag	ccccacccgc	180
tctggcccca	ccctcaccct	ccaacaaaga	tttatcaa	atgtgggatttt	cccatgagtc	240
tcaatattag	agtctcaacc	cccaataaat	ataggactgg	agatgtctct	gaggctcatt	300
ctgcc						305

<210> 129
 <211> 1181
 <212> DNA
 <213> Homo sapiens

<400> 129	
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gtttctcttct	agcttctttt tgatttcaaa tcaagactta cagggagagg gagcgataaa 180
cacaaactct	gcaagatgcc acaaggtcct cctttgacat cccaacaaa gaaggtagt 240
agtaatctcc	ccctttctgc cctgaaccaa gtggttcag taagtttcag ggctccagga 300
gacctgggca	tgcaggtgcc gatgaaacag tggatgaagag actcagtggc agtggcagtg 360
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ctcacaggga	gagccagaac acagcaagaa ctcatgatgac tggtagtatt accttcttca 660
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gttttttaca	atataaattaa ctggaacgct aaattctagc ctgttaatct ggctactgaa 780
aaaaaaaaa	tttttttttt ttcaaaaaac atagcttttag cttatttttt ttttctcttt 840
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caaagattta	tcaaatgtgg gattttccca tgagtctcaa tattagagtc tcaaccccca 1140
ataaatatag	gactggagat gtctctgagg ctcatctgc c
	1181

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 <211> 778
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<213> Homo sapiens

<400> 130

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ccaaactctt taaggacaag tacctagtct tatctatttc tagatcccc acattactca 120

gaaagttact ccataaatgt ttgtggaact gatttctatg tgaagacatg tgccccttca 180

ctctgttaac tagcattaga aaaacaaatc ttttgaaaag ttgtagtatg cccctaagag 240

cagtaacagt tcctagaaac tctctaaaat gcttagaaaa agatttattt taaattacct 300

ccccataaaa atgattggct ggcttatctt caccatcatg atagcatctg taattaactg 360

aaaaaaaaata attatgccat taaaagaaaa tcatccatga tcttgttcta acacctgcca 420

ctctagtact atatctgtca catggtctat gataaagtta tctagaaata aaaaagcata 480

caattgataa ttcaccaa atgtggagctt cagtatttta aatgtatatt aaaattaaat 540

tatttttaaag atcaaagaaa actttcgtca tactccgtat ttgataagga acaaatagga 600

agtgatgatga ctcaggtttg ccctgagggg atgggccatc agttgcaaat cgtggaattt 660

cctctgacat aatgaaaaga tgagggtgca taagttctct agtagggatga tgatataaaa 720

agccaccgga gcactccata aggcacaaac tttcagagac agcagagcac acaagctt 778

<210> 131

<211> 207

<212> DNA

<213> Homo sapiens

<400> 131

actccgtatt tgataaggaa caaataggaa gtgtgatgac tcagggttgc cctgagggga 60

tgggccatca gttgcaaata gtggaatttc ctctgacata atgaaaagat gaggggtgcat 120

aagttctcta gtagggatgat gatataaaaa gccaccggag cactccataa ggcacaaact 180

ttcagagaca gcagagcaca caagctt 207

<210> 132

<211> 645

<212> DNA

<213> Homo sapiens

<400> 132

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ttcctgaggc ctcaagcctg ccaccaagcc ccagctcct tctccccgca gggcccaaac 120

acaggcctca ggactcaaca cagcttttcc ctccaacccc gttttctctc cctcaacgga 180

ctcagcttgc tgaagccct cccagttcta gttctatctt tttcctgcat cctgtctgga 240

agttagaagg aaacagacca cagacctggg ccccaaaaga aatggaggca atagggtttg 300

aggggcatgg ggacgggggt cagcctccag ggtcctacac acaaatcagt cagtggccca 360

gaagaccccc ctcggaatcg gagcagggag gatggggagt gtgaggggta tccttgatgc 420
 ttgtgtgtcc ccaactttcc aaatccccgc ccccgcgatg gagaagaaac cgagacagaa 480

ggtgcagggc ccactaccgc ttcctccaga tgagctcatg ggtttctcca ccaaggaagt 540

tttccgctgg ttgaatgatt ctttccccgc cctcctctcg cccagggac atataaaggc 600

agttgttggc acaccagcc agcagacgct ccctcagcaa ggaca 645

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 <213> Homo sapiens

<400> 133
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ctccagctca caccacagct gctcaaccac ctctctctg aattgactgt cccttctttg 120

gaactctagg cctgacccca ctccctggcc ctcccagccc acgattcccc tgaccogact 180

ccctttccca gaactcagtc gcctgaaccc ccagcctgtg gttctctcct aggcctcagc 240

ctttcctgcc tttgactgaa acagcagtat cttctaagcc ctgggggctt ccccgggccc 300

cagccccgac ctagaacccg cccgctgcct gccacgctgc cactgccgct tcctctataa 360

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ctccttgggc tgcccgtgct tcgtgctttg gactacc 457

<210> 134
 <211> 973
 <212> DNA
 <213> Homo sapiens

<400> 134
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ggctcagaat atgtctaagc aattgaggaa tgtctcagaa aacgtggggc tagtgtgcca 120

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 gctggtgtat aaaatgctct atatatgcc attatcaatt tcctttcatg ttcagcattt 240
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cgggtgggaga ctgaggccgc cttggcgggg cgggacgaga ctctccgag gtcgggaaag 540
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21